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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 22 18:00:40 1999; MasPar time 7.92 Seconds
 830.441 Million cell updates/sec

Tabular output not generated.

Title: >US-09-162-597-3
 Description: (1-245) from US09162597.pep
 Perfect Score: 1940

Sequence: 1 MTLHFGNCFALAYFPYFIT.....GLVSQTLMYLFPASLQLVLVK 245

Scoring table: PAM 150
 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: swiss-prot35
 1:swissprot

Statistics: Mean 47.613; Variance 90.624; scale 0.525

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	118	6.1	572	1	PT1_MYCPN	PHOSPHOENOLPYRUVATE-PR	2.41e-03		
2	113	5.8	215	1	CYB6_ORYSA	CYTOCHROME B6 (EC 1.10	1.21e-02		
3	113	5.8	215	1	CYB6_MAIZE	CYTOCHROME B6 (EC 1.10	1.21e-02		
4	113	5.8	215	1	CYB6_WHEAT	CYTOCHROME B6 (EC 1.10	1.21e-02		
5	111	5.7	215	1	CYB6_TOBAC	CYTOCHROME B6 (EC 1.10	2.27e-02		
6	106	5.5	167	1	NU6M_APIME	NADH-UBIQUINONE OXIDOR	1.07e-01		
7	107	5.5	215	1	CYB6_SYNPI7	CYTOCHROME B6 (EC 1.10	7.89e-02		
8	107	5.5	215	1	CYB6_CHLRE	CYTOCHROME B6 (EC 1.10	7.89e-02		
9	106	5.5	215	1	CYB6_NOSSP	CYTOCHROME B6 (EC 1.10	1.07e-01		
10	106	5.5	215	1	CYB6_SPIOL	CYTOCHROME B6 (EC 1.10	1.07e-01		
11	105	5.4	215	1	CYB6_MARPO	CYTOCHROME B6 (EC 1.10	1.45e-01		
12	104	5.4	215	1	CYB6_ODOSI	CYTOCHROME B6 (EC 1.10	1.97e-01		
13	104	5.4	215	1	CYB6_PORPU	CYTOCHROME B6 (EC 1.10	1.97e-01		
14	105	5.4	222	1	CYB6_SYNPI2	CYTOCHROME B6 (EC 1.10	1.45e-01		
15	103	5.3	215	1	CYB6_CYAPA	CYTOCHROME B6 (EC 1.10	2.66e-01		
16	103	5.3	222	1	CYB6_PROHO	CYTOCHROME B6 (EC 1.10	2.66e-01		
17	103	5.3	222	1	CYB6_SYNPI3	CYTOCHROME B6 (EC 1.10	2.66e-01		
18	102	5.3	552	1	CYHR_CANMA	CYCLOHEXIMIDE RESISTAN	3.58e-01		
19	101	5.2	215	1	CYB6_PINTH	CYTOCHROME B6 (EC 1.10	4.81e-01		
20	101	5.2	365	1	NQ08_THETH	NADH-UBIQUINONE OXIDOR	4.81e-01		
21	101	5.2	430	1	RFBX_SALTY	PUTATIVE O-ANTIGEN TRA	4.81e-01		
22	101	5.2	570	1	PT1_BACSU	PHOSPHOENOLPYRUVATE-PR	4.81e-01		
23	99	5.1	215	1	CYB6_CHLVI	CYTOCHROME B6 (EC 1.10	8.64e-01		

24	99	5.1	215	1	CYB6_CHLPR	CYTOCHROME B6 (EC 1.10	8.64e-01		
25	98	5.1	422	1	SYT2_RAT	SYNAPTOTAGMIN II.	1.15e+00		
26	98	5.1	422	1	SYT2_MOUSE	SYNAPTOTAGMIN II.	1.15e+00		
27	98	5.1	573	1	PT1_MYCCA	PHOSPHOENOLPYRUVATE-PR	1.15e+00		
28	98	5.1	592	1	ODP2_DICDI	DHYDROLIPOAMIDE ACETY	1.15e+00		
29	97	5.0	304	1	G6PI_CALPI	GLUCOSE-6-PHOSPHATE IS	1.54e+00		
30	97	5.0	601	1	KEFB_ECOLI	GLUTATHIONE-REGULATED	1.54e+00		
31	96	4.9	379	1	CYB_CRAGR	CYTOCHROME B (EC 1.10.	2.04e+00		
32	95	4.9	379	1	CYB_CRAGY	CYTOCHROME B (EC 1.10.	2.71e+00		
33	95	4.9	775	1	UL87_HSV7J	PROTEIN U58.	2.71e+00		
34	96	4.9	1323	1	HST6_CANAL	ATP-DEPENDENT PERMEASE	2.04e+00		
35	95	4.9	1353	1	CYA9_MOUSE	ADENYLATE CYCLASE, TYP	2.71e+00		
36	94	4.8	151	1	Y4JR_RHISN	HYPOTHETICAL 17.3 KD P	3.59e+00		
37	94	4.8	342	1	ISIA_SYN3	IRON-STRESS INDUCED CH	3.59e+00		
38	94	4.8	379	1	CYB_CRAGG	CYTOCHROME B (EC 1.10.	3.59e+00		
39	93	4.8	382	1	LPXB_ECOLI	LIPID-A-DISACCHARIDE S	4.74e+00		
40	94	4.8	491	1	Y225_MYCPN	HYPOTHETICAL PROTEIN M	3.59e+00		
41	94	4.8	578	1	YFCU_ECOLI	HYPOTHETICAL OUTER MEM	3.59e+00		
42	93	4.8	637	1	YA07_SCHPO	PUTATIVE 73.4. KD TRANS	4.74e+00		
43	94	4.8	842	1	AMPN_LACDL	AMINOPEPTIDASE N (EC 3	3.59e+00		
44	93	4.8	1035	1	EPA6_MOUSE	EPHRIN TYPE-A RECEPTOR	4.74e+00		
45	94	4.8	2470	1	TOR1_YEAST	PHOSPHATIDYLINOSITOL 3	3.59e+00		

ALIGNMENTS

RESULT	1	ID	PT1_MYCPN	STANDARD;	PRT;	572 AA.
AC	P75168;	DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)	DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (EC 2.7.3.9)	DE	(PHOSPHOTRANSFERASE SYSTEM, ENZYME I).			
GN	PTSI.	OS	MYCOPLASMA PNEUMONIAE.			
OC	PROKARYOTA; Tenericutes; Mollicutes; Mycoplasma; Mycoplasmatales;	OC	MYCOPLASMATACEAE.			
RN	[1]	RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 29342 / M129;	RX	MEDLINE; 97105885.			
RA	HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,	RA	HERRMANN R.;			
RL	NUCLEIC ACIDS RES. 24:4420-4449(1996).	CC	-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. ENZYME I TRANSFERS THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE (PEP) TO THE PHOSPHORYL CARRIER PROTEIN (HPR). ENZYME I IS COMMON TO ALL PTS (BY SIMILARITY).			
CC	-!- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + PROTEIN N-PHOSPHOHISTIDINE - PYRUVATE + PROTEIN N-PHOSPHOHISTIDINE.	CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.	CC	-!- SIMILARITY: TO OTHER PEP-UTILIZING ENZYMES.			
DR	EMBL: AE000021; G1673880; -.	DR	PROSITE; PS00370; PEP_ENZYMES_PHOS_SITE; 1.			
DR	PROSITE; PS00742; PEP_ENZYMES_2; 1.	KW	PHOSPHOTRANSFERASE SYSTEM; TRANSFERASE; KINASE; SUGAR TRANSPORT;			
KW	PHOSPHORYLATION.	FT	MOD_RES 190 190 PHOSPHORYLATION (BY SIMILARITY).			
SQ	SEQUENCE 572 AA; 63950 MW; 24ED53DF CRC32;	Query	Match 6.1%; Score 118; DB 1; Length 572;			
		Best Local Similarity 28.8%; Pred. No. 2.41e-03;				
		Matches 23; Conservative 26; Mismatches 25; Indels 6; Gaps 6;				
Db	446 SIGTN-DLIQYSFAADRMRNNKNSV-LYQPLNPKLKLIVLTIEGGKVNDIWIGMCGEMAG 503	: :	Qy	136 SIDSNISLVHYIVASAQWMTRYDLYHNFRPVLMLPLSVYKAFVMTFVHLCS-LGS 194		
Db	504 -EPL-AIPLLGL-GLKEFS 520	:: : : :				

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Qy 195 WARLDARAVVTGLLALKHFG 214

RESULT 2
 ID CYB6_ORYSA STANDARD; PRT; 215 AA.
 AC P12123;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).
 GN PETB.

OS ORYZA SATIVA (RICE).

OG CHLOROPLAST.

OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
 OC CYPERALES; GRAMINEAE.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA SUGIURA M.;

RL SUBMITTED (JUL-1989) TO EMBL/GENBANK/DDJB DATA BANKS.

RN [2]

RP COMPLETE GENOME.

RX MEDLINE; 89364698.

RA HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M.,

RA MORI M., KONDO C., HONJI Y., SUN C.-R., MENG B.-Y., LI Y.-Q.,

RA KANNO A., NISHIZAWA Y., HIRAI A., SHINOZAKI K., SUGIURA M.;

RL MOL. GEN. GENET. 217:185-194(1989).

RN [3]

RP SEQUENCE FROM N.A.

RA COTE J.C., WU N.H., WU R.;

RL PLANT MOL. BIOL. 11:873-874(1988).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART

CC OF THE CHLOROPLASTIC RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN =

CC PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

CC BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,

CC 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; X15901; G669082; -.

DR EMBL; M35995; G343209; -.

DR PIR; JQ0256; CBR26.

DR MENDEL; 4313; ORYSA; PETB; 1.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

SQ SEQUENCE 215 AA; 24182 MW; 086A69C5 CRC32;

Query Match 5.8%; Score 113; DB 1; Length 215;
 Best Local Similarity 23.5%; Pred. No. 1.21e-02;
 Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTEANFGWLI-R-SV-HRWSASMMVLMILHVFRVYLTCGGFKKP 113
 | : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 132 YIQMSIDSNSNLVHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWWTGVVLAVLTASFGVTGYS 137
 | : | : | : | : | : | : |

Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 3
 ID CYB6_MAIZE STANDARD; PRT; 215 AA.
 AC P05642;
 DT 01-NOV-1988 (REL. 09, CREATED)

DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE CYTOCHROME B6 (EC 1.10.99.1).
 GN PETB.
 OS ZEA MAYS (MAIZE).
 OG CHLOROPLAST.
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
 OC CYPERALES; GRAMINEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88210525.
 RA ROCK C.D., BARKAN A., TAYLOR W.C.;
 RL Curr. Genet. 12:69-77(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95395841.
 RA MAIER R.M., NECKERMAN K., IGLOI G.L., KOESSEL H.;
 RL J. Mol. Biol. 251:614-628(1995).
 CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART
 CC OF THE CHLOROPLASTIC RESPIRATORY CHAIN.
 CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN =
 CC PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,
 CC 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.
 CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.
 DR EMBL; X05422; G311718; -.
 DR EMBL; X86563; G902251; ALT_SEQ.
 DR PIR; S08592; CB2M6R.
 DR MAZEDB; 56334; -.
 DR MENDEL; 4315; ZEAMA; PETB; 1.
 DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 KW ELECTRON TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.
 FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 SQ SEQUENCE 215 AA; 24180 MW; CBAB4737 CRC32;

Query Match 5.8%; Score 113; DB 1; Length 215;
 Best Local Similarity 23.5%; Pred. No. 1.21e-02;
 Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTEANFGWLI-R-SV-HRWSASMMVLMILHVFRVYLTCGGFKKP 113
 | : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 132 YIQMSIDSNSNLVHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWWTGVVLAVLTASFGVTGYS 137
 | : | : | : | : | : | : |

Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 4
 ID CYB6_WHEAT STANDARD; PRT; 215 AA.
 AC P12362;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
 DE CYTOCHROME B6 (EC 1.10.99.1).
 GN PETB.
 OS TRITICUM AESTIVUM (WHEAT), AND HORDEUM VULGARE (BARLEY).
 OG CHLOROPLAST.
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
 OC CYPERALES; GRAMINEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=WHEAT; STRAIN=CV. MARDLER;
 RX MEDLINE; 91329710.

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Db 69 LSGMLIM 75

::|:: :

Qy 204 VTGLLAL 210

RESULT 7

ID CYB6_SYNTP7 STANDARD; PRT; 215 AA.

AC Q54711;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS SYNECHOCOCCUS SP. (STRAIN PCC 7942) (ANACYSTIS NIDULANS R2).

OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;

OC CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES.

RN [1]

RP SEQUENCE FROM N.A.

RA NEWNAN J., KARAKAYA H., SCANLAN D.J., CARR N.G., MANN N.H.;

RL SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDJB DATA BANKS.

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART OF THE CYANOBACTERIAL RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN = PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,

CC 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; U33285; G988289; -.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

(BY SIMILARITY).

SQ SEQUENCE 215 AA; 24357 MW; 38B90BD7 CRC32;

Query Match 5.5%; Score 107; DB 1; Length 215;

Best Local Similarity 23.7%; Pred. No. 7.89e-02;

Matches 18; Conservative 20; Mismatches 32; Indels 6; Gaps 6;

Db 57 YYKPTVAEAYSSVQFIMNQVNFGWLI-R-SI-HRWSASMMVLMILHVFRVLGGFKRP 113

| : :: ||::|: |::| : | :::: |::| |::| : | :

Qy 132 YIQMSIDSNSLNVHYIVASAQV-WMITRYDLYHNFRPAVL-LLMPLSVYKAFVMETFVHL 189

Db 114 REL-TWGVVMAVIT 128

| : | ||::|

Qy 190 CSLGSWARLDARAVVT 205

RESULT 8

ID CYB6_CHLRE STANDARD; PRT; 215 AA.

AC Q00471;

DT 01-DEC-1992 (REL. 24, CREATED)

DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS CHLAMYDOMONAS REINHARDTII.

OG CHLOROPLAST.

OC EUKARYOTA; PLANTAE; PHYCOPHYTA; CHLOROPHYTA (GREEN ALGAE);

OC CHLOROPHYCEAE; VOLVOCALES; CHLAMYDOMONADACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 92256821.

RA HUANG C., LIU X.-Q.;

RL PLANT MOL. BIOL. 18:985-988(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=137C;

RX MEDLINE; 91285146.

RA BUESCHLEN S., CHOQUET Y., KURAS R., WOLLMAN F.A.;

RL FEBS LETT. 284:257-262(1991).

RN [3]

RP CHARACTERIZATION.

RC STRAIN=WT12;

RX MEDLINE; 96094329.

RA PIERRE Y., BREYTON C., KRAMER D., POPOT J.-L.;

RL J. BIOL. CHEM. 270:29342-29349(1995).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART OF THE CHLOROPLASTIC RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN = PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- PTM: THE N-TERMINAL IS BLOCKED.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; X62905; G12499; -.

DR EMBL; X72918; G288909; -.

DR PIR; S16917; S16917.

DR PIR; S21253; S21253.

DR MENDEL; 4312; CHLRE; PETB; 1.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON-TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

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FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

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FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

(BY SIMILARITY).

FT METAL

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,
 CC 17 KD POLYPEPTIDE (PETO), CYTOCHROME F AND THE RIESKE PROTEIN.
 CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.
 DR EMBL; J03967; G145023; -.

DR PIR; A30807; A30807.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)
 (BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)
 (BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)
 (BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)
 (BY SIMILARITY).

SQ SEQUENCE 215 AA; 24259 MW; DEAE4993 CRC32;

Query Match 5.5%; Score 106; DB 1; Length 215;

Best Local Similarity 25.0%; Pred. No. 1.07e-01;

Matches 19; Conservative 18; Mismatches 33; Indels 6; Gaps 6;

Db 57 YYKPTVAEAFSSVEIMNEVNGWLI-R-SI-HRWSASMMVLMMLHVFRVYLTGGFKKP 113
 | :: :: ||::: |::| : | :::: ||::| ||:: :: |

Qy 132 YIQMSIDSNIISLVHYIVASAQW-WMTRYDLYHNPRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWVSGVILAVIT 128
 | :| ||::|

Qy 190 CSLGSWARLDARAVVT 205

RESULT 10

ID CYB6_SPIOL STANDARD; PRT; 215 AA.

AC P00165;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)

DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS SPINACIA OLERACEA (SPINACH).

OG CHLOROPLAST.

OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;

OC CARYOPHYLLALES; CHENOPODIACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 88194670.

RA WESTHOFF P., FARCHAUS J.W., HERRMANN R.G.;

RL CURR. GENET. 11:165-169(1986).

RN [2]

RP SEQUENCE FROM N.A.

RA HEINEMAYER W., ALT J., HERRMANN R.G.;

RL CURR. GENET. 8:543-549(1984).

RN [3]

RP SEQUENCE.

RX MEDLINE; 84144766.

RA WIDGER W.R., CRAMER W.A., HERRMANN R.G., TREBST A.;

RL PROC. NATL. ACAD. SCI. U.S.A. 81:674-678(1984).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART
 CC OF THE CHLOROPLASTIC RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN =
 CC PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,
 CC 17 KD POLYPEPTIDE (PETO), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; X07106; G12285; -.

DR PIR; A00161; CBSP6.

DR PIR; S00429; S00429.

DR MENDEL; 2553; SPIOL;PETB;1.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND).
 FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND).
 FT CONFLICT 108 109 MISSING (IN REF. 3).
 FT CONFLICT 188 188 MISSING (IN REF. 3).
 SQ SEQUENCE 215 AA; 24166 MW; 35EE50AD CRC32;

Query Match 5.5%; Score 106; DB 1; Length 215;
 Best Local Similarity 22.7%; Pred. No. 1.07e-01;
 Matches 15; Conservative 21; Mismatches 24; Indels 6; Gaps 6;

Db 57 YYRPTVTDASFVQYIMTEVNGWLI-R-SV-HRWSASMMVLMMLHVFRVYLTGGFKKP 113
 | : :: :: ||::: |::| : | :::: ||::| :::: |

Qy 132 YIQMSIDSNIISLVHYIVASAQW-WMTRYDLYHNPRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TW 118
 | :|

Qy 190 CSLGSW 195

RESULT 11

ID CYB6_MARPO STANDARD; PRT; 215 AA.

AC P06248;

DT 01-JAN-1988 (REL. 06, CREATED)

DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)

DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS MARCHANTIA POLYMORPHA (LIVERWORT).

OG CHLOROPLAST.

OC EUKARYOTA; PLANTA; EMBRYOPHYTA; BRYOPHYTA; HEPATICOPSIDA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 89068687.

RA FUKUZAWA H., KOKCHI T., SANO T., SHIRAI H., UMESONO K., INOKUCHI H.,
 RA OZEKI H., OHYAMA K.;

RL J. MOL. BIOL. 203:333-351(1988).

RN [2]

RP COMPLETE GENOME.

RA OHYAMA K., FUKUZAWA H., KOKCHI T., SHIRAI H., SANO T., SANO S.,

RA UMESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,

RA OZEKI H.;

RL NATURE 322:572-574(1986).

RN [3]

RP SEQUENCE FROM N.A.

RA FUKUZAWA H., YOSHIDA T., KOKCHI T., OKUMURA T., SAWANO Y., OHYAMA K.;

RL FEBS LETT. 220:61-66(1987).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART
 CC OF THE CHLOROPLASTIC RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN =
 CC PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,
 CC 17 KD POLYPEPTIDE (PETO), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; X04465; E122080; -.

DR PIR; A00163; CBLV6.

DR PIR; S01552; S01552.

DR PIR; S02432; S02432.

DR MENDEL; 2551; MARPO;PETB;1.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND).
 FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND).

SQ SEQUENCE 215 AA; 24307 MW; A8EDE412 CRC32;

Query Match 5.4%; Score 105; DB 1; Length 215;

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Best Local Similarity 22.7%; Pred. No. 1.45e-01;
 Matches 15; Conservative 21; Mismatches 24; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTEVNFGWLI-R-SI-HRWSASMMVLMILHFRVYLTTGGFKKP 113
 | : :: :: ||::| : | : | :::: ||::| :::: |

Qy 132 YIQMSIDSNISLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TW 118
 | : |

Qy 190 CSLGSW 195

RESULT 12

ID CYB6_ODOSI STANDARD; PRT; 215 AA.

AC P49488;

DT 01-FEB-1996 (REL. 33, CREATED)

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS ODONTELLA SINENSIS.

OG CHLOROPLAST.

OC EUKARYOTA; PLANTA; PHYCOPHYTA; BACILLARIOPHYTA (DIATOMS).

RN [1]

RP SEQUENCE FROM N.A.

RA KOWALLIK K.V., STOEBE B., SCHAFFRAN I., KROTH-PANCIC P., FREIER U.;

RL PLANT MOL. BIOL. REP. 13:336-342(1995).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART OF THE CHLOROPLASTIC RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN = PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; U38804; G1276807; -

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

SQ SEQUENCE 215 AA; 23923 MW; 79C43185 CRC32;

Query Match 5.4%; Score 104; DB 1; Length 215;

Best Local Similarity 26.3%; Pred. No. 1.97e-01;

Matches 20; Conservative 19; Mismatches 31; Indels 6; Gaps 6;

Db 57 YYRPSVVDAFASVEYIMTSVNFGLI-R-SI-HRWSASMMVLMILHFRVYLTTGGFKKP 113
 | : | : :: ||::| : | : | :::: ||::| :::: |

Qy 132 YIQMSIDSNISLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWTVGVILAVVT 128
 | : | ||||

Qy 190 CSLGSWARLDARAVVT 205

RESULT 13

ID CYB6_PORPU STANDARD; PRT; 215 AA.

AC P51341;

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS PORPHYRA PURPUREA.

OG CHLOROPLAST.

OC EUKARYOTA; PLANTA; PHYCOPHYTA; RHODOPHYTA (RED ALGAE).

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AVONPORT;

RA REITH M.E., MUNHOLLAND J.;

RL PLANT MOL. BIOL. REP. 13:333-335(1995).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART OF THE CHLOROPLASTIC RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN = PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; U38804; G1276807; -

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; CHLOROPLAST; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

SQ SEQUENCE 215 AA; 24224 MW; 9F90E552 CRC32;

Query Match 5.4%; Score 104; DB 1; Length 215;

Best Local Similarity 22.7%; Pred. No. 1.97e-01;

Matches 15; Conservative 20; Mismatches 25; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTDVNFGWLI-R-SI-HRWSASMMVLMILHFRVYLTTGGFKKP 113
 | : :: :: ||::| : | : | :::: ||::| :::: |

Qy 132 YIQMSIDSNISLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TW 118
 | : |

Qy 190 CSLGSW 195

RESULT 14

ID CYB6_SYNTP2 STANDARD; PRT; 222 AA.

AC P28056;

DT 01-AUG-1992 (REL. 23, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)

DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRUPPLICATUM).

OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;

OC CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCcales.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93043038.

RA BRAND S.N., TAN X., WIDGER W.R.;

RL PLANT MOL. BIOL. 20:481-491(1992).

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART OF THE CYANOBACTERIAL RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN = PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; X63049; G38963; -

DR PIR; S18123; S18123.

DR PIR; S26193; S26193.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 93 93 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

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FT METAL 107 107 IRON 2 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 FT METAL 194 194 IRON 2 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 FT METAL 209 209 IRON 1 (HEME AXIAL LIGAND)
 FT (BY SIMILARITY).
 SQ SEQUENCE 222 AA; 25179 MW; 7F5AB232 CRC32;

Search completed: Fri Jan 22 18:00:58 1999
 Job time: 18 secs.

Query Match 5.4%; Score 105; DB 1; Length 222;
 Best Local Similarity 21.2%; Pred. No. 1.45e-01;
 Matches 14; Conservative 21; Mismatches 25; Indels 6; Gaps 6;

Db 64 YYKPTVAEAFTSVQYIMNEVNFGWLI-R-SI-HRWSASMMVLMMILHIFRVYLTGGFKRP 120
 | :: :: ||::| :||| :| :| ::||:| ::| :| :

Qy 132 YIQMSIDSNSLIVHYIVASAQV-WMTRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 121 REL-TW 125
 | :|

Qy 190 CSLGSW 195

RESULT 15
 ID CYB6_CYAPA STANDARD; PRT; 215 AA.

AC P48121;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT Q1-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE CYTOCHROME B6 (EC 1.10.99.1).

GN PETB.

OS CYANOPHORA PARADOXA.

OG CYANELLE.

OC EUKARYOTA; PLANTA; PHYCOPHYTA; GLAUCOPHYTA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LB555 / PRINGSHEIM;

RA STIREWALT V.L., MICHALOWSKI C.B., LUFPFHARDT W., BOHNERT H.J.,

RA BRYANT D.A.;

RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -!- FUNCTION: COMPONENT OF THE CYTOCHROME B6/F COMPLEX WHICH IS PART
 CC OF THE CYANELLE RESPIRATORY CHAIN.

CC -!- CATALYTIC ACTIVITY: PLASTOQUINOL-1 + 2 OXYDIZED PLASTOCYANIN =
 CC PLASTOQUINONE + 2 REDUCED PLASTOCYANIN.

CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.

CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6,
 CC 17 KD POLYPEPTIDE (PETD), CYTOCHROME F AND THE RIESKE PROTEIN.

CC -!- SIMILARITY: WITH THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

DR EMBL; U30821; G1016119; .

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW ELECTRON TRANSPORT; HEME; CYANELLE; PHOTOSYNTHESIS; TRANSMEMBRANE.

FT METAL 86 86 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 100 100 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 187 187 IRON 2 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

FT METAL 202 202 IRON 1 (HEME AXIAL LIGAND)

FT (BY SIMILARITY).

SQ SEQUENCE 215 AA; 24188 MW; 1042B361 CRC32;

Query Match 5.3%; Score 103; DB 1; Length 215;
 Best Local Similarity 23.7%; Pred. No. 2.66e-01;
 Matches 18; Conservative 21; Mismatches 31; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFASVQYIMTDVNFGWLI-R-ST-HRWSASMMVLMMILHIFRVYLTGGFKP 113
 | :: :: :: ||::| :||| :| :| ::||:| ::| :| :

Qy 132 YIQMSIDSNSLIVHYIVASAQV-WMTRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWVVGVLAVIT 128
 | :| |||:

Qy 190 CSLGSWARLDARAVVT 205


 (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 22 18:00:03 1999; MasPar time 11.44 Seconds
 802.613 Million cell updates/sec

Tabular output not generated.

Title: >US-09-162-597-3
 Description: (1-245) from US09162597.pep
 Perfect Score: 1940

Sequence: 1 MTLFHFGNCFALAYFPYFIT.....GLVSQTLMYLFPASLQLVLVK 245

Scoring table: PAM 150
 Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir58
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.371; Variance 103.911; scale 0.446

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	118	6.1		572	2	S73541		phosphotransferase sy	2.05e-02
2	113	5.8		215	1	CBZM6R		plastoquinol-plastoc	8.32e-02
3	113	5.8		215	2	S14961		plastoquinol-plastoc	8.32e-02
4	113	5.8		215	1	CBR26		plastoquinol-plastoc	8.32e-02
5	113	5.8		215	1	S09186		plastoquinol-plastoc	8.32e-02
6	113	5.8		232	1	S04149		plastoquinol-plastoc	8.32e-02
7	113	5.8		234	2	S58581		plastoquinol-plastoc	8.32e-02
8	111	5.7		215	1	CBNT6		plastoquinol-plastoc	1.44e-01
9	106	5.5		167	2	S52970		NADH dehydrogenase (u	5.58e-01
10	107	5.5		215	1	S21253		plastoquinol-plastoc	4.27e-01
11	106	5.5		215	1	A30807		plastoquinol-plastoc	5.58e-01
12	106	5.5		215	1	CBSP6		plastoquinol-plastoc	5.58e-01
13	105	5.4		212	2	B69031		conserved hypothetical	7.28e-01
14	105	5.4		215	1	CBLV6		plastoquinol-plastoc	7.28e-01
15	104	5.4		215	2	S73262		cytochrome b6 - red a	9.48e-01
16	104	5.4		215	2	S78307		plastoquinol-plastoc	9.48e-01
17	105	5.4		222	2	S26193		plastoquinol-plastoc	7.28e-01
18	104	5.4		310	2	D70139		conserved hypothetical	9.48e-01
19	103	5.3		222	2	S76297		hypothetical protein	1.23e+00
20	103	5.3		222	2	S22470		plastoquinol-plastoc	1.23e+00
21	102	5.3		552	2	JC1173		cycloheximide resista	1.60e+00
22	101	5.2		430	2	S15308		hypothetical protein	2.07e+00
23	101	5.2		570	1	C46238		phosphotransferase sy	2.07e+00

24	99	5.1	215	1	CBKL6P	plastoquinol-plastoc	3.46e+00
25	99	5.1	247	2	G71009	hypothetical protein	3.46e+00
26	98	5.1	351	2	S58745	NADH dehydrogenase (u	4.46e+00
27	99	5.1	363	2	H69142	perosamine synthetase	3.46e+00
28	98	5.1	422	1	A55417	synaptotagmin II - mo	4.46e+00
29	98	5.1	422	1	BMRT2Y	synaptotagmin II - ra	4.46e+00
30	99	5.1	2206	2	JC5280	voltage-dependent cal	3.46e+00
31	97	5.0	87	2	H70079	hypothetical protein	5.74e+00
32	97	5.0	172	2	G69467	CDP-diacylglycerol--g	5.74e+00
33	97	5.0	598	2	S75728	hypothetical protein	5.74e+00
34	97	5.0	601	2	A65129	glutathione-regulated	5.74e+00
35	96	4.9	153	2	B69434	benzodiazepine recept	7.37e+00
36	95	4.9	162	2	F71319	hypothetical protein	9.44e+00
37	95	4.9	377	2	C69758	amino acid transporte	9.44e+00
38	95	4.9	442	2	S50332	NADH dehydrogenase (u	9.44e+00
39	96	4.9	683	1	A41785	system b(0,+)- amino a	7.37e+00
40	95	4.9	1353	2	JC4279	adenylate cyclase (EC	9.44e+00
41	94	4.8	239	2	D71215	hypothetical protein	1.21e+01
42	94	4.8	491	2	S73844	hypothetical protein	1.21e+01
43	94	4.8	578	2	H65006	hypothetical protein	1.21e+01
44	94	4.8	1415	2	S52267	DNA polymerase III -	1.21e+01
45	94	4.8	2470	2	S57085	1-phosphatidylinosito	1.21e+01

ALIGNMENTS

RESULT	1
ENTRY	S73541 #type complete
TITLE	phosphotransferase system enzyme I (EC 2.7.3.9) - Mycoplasma pneumoniae (SGC3)
ALTERNATE_NAMES	phosphoenolpyruvate--protein phosphotransferase; protein C12_orf572
ORGANISM	#formal_name Mycoplasma pneumoniae
DATE	27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 17-Jul-1998
ACCESSIONS	S73541
REFERENCE	S73327
#authors	Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
#journal	Nucleic Acids Res. (1996) 24:4420-4449
#title	Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
#cross-references	MUID:97105885
#accession	S73541
	##status nucleic acid sequence not shown; translation not shown
	##molecule_type DNA
	##residues 1-572 ##label HIM
	##cross-references EMBL:AE000021; GB:U00089; NID:g1673871; PID:g1673880
	##experimental_source ATCC 29342
	##note the nucleotide sequence was submitted to the EMBL Data Library, November 1996
GENETICS	
#gene	ptsI
#genetic_code	SGC3
CLASSIFICATION	#superfamily phosphotransferase system enzyme I; phosphotransferase system enzyme I homology
KEYWORDS	phosphotransferase; sugar transport system
FEATURE	4-557 #domain phosphotransferase system enzyme I homology #label PT1
SUMMARY	#length 572 #molecular-weight 63950 #checksum 7396
Query Match	6.1%; Score 118; DB 2; Length 572;
Best Local Similarity	28.8%; Pred. No. 2.05e-02;
Matches	23; Conservative 26; Mismatches 25; Indels 6; Gaps 6;
Db	446 SIGTN-DLIQYSFAADRNMKNVSY-LYQPLNPALLKLIYLTIIEGGKVNDIWTGMCDEMAG 503 : : : : : : : : : : : : : : :
Qy	136 SIDSNSILVHYIVASAQVWMITRYDLYHNFRPAVLLLMPLSVYKAFVMETFVHLCS-LGS 194 :: : : : : : : : : : : : : : : :
Db	504 -EPL-AIPLLGL-GLKEFS 520 :: : : :
Qy	195 WARLDARAVVTGLLALKHFG 214

RESULT 2

ENTRY CBZM6R #type complete

TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
cytochrome b6 - maize chloroplast

ORGANISM #formal_name chloroplast Zea mays #common_name maize

DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
05-Sep-1997

ACCESSIONS S08592

REFERENCE #authors Rock, C.D.; Barkan, A.; Taylor, W.C.
#journal Curr. Genet. (1987) 12:69-77
#title The maize plastid psbB-psbF-petB-petD gene cluster: spliced and unspliced petB and petD RNAs encode alternative products.

#cross-references MUID:88210525

#accession S08592
##molecule_type DNA
##residues 1-215 ##label ROC

#cross-references EMBL:X05422; NID:g12434; PID:g311718

GENETICS

#gene	petB
#genome	chloroplast
#introns	2/3

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology

KEYWORDS chloroplast; chromoprotein; electron transfer; heme; iron; oxidoreductase; photosynthesis; thylakoid

FEATURE

15-215	#domain cytochrome b6 homology ##label CB6\
86,202	#binding_site heme iron (His) (axial ligands) #status predicted
100,187	#binding_site heme iron (His) (axial ligands) #status predicted

SUMMARY #length 215 #molecular_weight 24180 #checksum 9478

Query Match 5.8%; Score 113; DB 1; Length 215;
Best Local Similarity 23.5%; Pred. No. 8.32e-02;
Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTEANPGWLI-R-SV-HRWSASMMVLLMMILHFRVYLTTGGFKKP 113
| : :: | : ||:: | : | | : | :: | : | : | : | : | : |

Qy 132 YIQMSIDSNSIISLVHYIVASAQV-WMITRDLYHNFRPAVL-LLMPLSVKAFVMETFVHL 189

Db 114 REL-TWVTGVVLAVLTASFPGVTGYS 137
| : | | : | : | : |

Qy 190 CSLGSWARLDARAVVTGLALKHFG 214

RESULT 3

ENTRY S14961 #type complete

TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
cytochrome b6 - wheat chloroplast

ALTERNATE_NAMES cytochrome b563

ORGANISM #formal_name chloroplast Triticum aestivum #common_name common wheat

DATE 08-Jun-1994 #sequence_revision 03-Aug-1995 #text_change
24-Apr-1998

ACCESSIONS S14961

REFERENCE #authors Hird, S.M.; Wilson, R.J.; Dyer, T.A.; Gray, J.C.
#journal Plant Mol. Biol. (1991) 16:745-747
#title Nucleotide sequence of the wheat chloroplast petB and petD genes encoding apocytochrome b-563 and subunit IV of the cytochrome bf complex.

#cross-references MUID:91329710

#accession S14961
##status preliminary
##molecule_type DNA
##residues 1-215 ##label HIR

#cross-references EMBL:X54751; NID:g12361; PID:g12363

GENETICS

#gene	petB
#map_position	CP1232-71237,72049-72690
#genome	chloroplast
#introns	2/3

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology

KEYWORDS chloroplast; chromoprotein; electron transfer; heme; iron; oxidoreductase; photosynthesis; thylakoid

FEATURE

15-215	#domain cytochrome b6 homology ##label CB6\
86,202	#binding_site heme iron (His) (axial ligands) #status predicted
100,187	#binding_site heme iron (His) (axial ligands) #status predicted

SUMMARY #length 215. #molecular_weight 24182 #checksum 9304

RESULT 4

ENTRY CBRZ6 #type complete

TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
cytochrome b6 - rice chloroplast

ORGANISM #formal_name chloroplast Oryza sativa #common_name rice

DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
18-Jul-1997

ACCESSIONS JQ0256; S05136

REFERENCE #authors Shimada, H.; Whittier, R.F.; Hiratsuka, J.; Maeda, Y.; Hirai, A.; Sugiura, M.
#submission submitted to JIPID, December 1989
#accession JQ0256
##molecule_type DNA
##residues 1-215 ##label SHI
##experimental_source cv. Nihonbare

REFERENCE S05080
#authors Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kondo, C.; Honji, Y.; Sun, C.R.; Meng, B.Y.; Li, Y.Q.; Kanno, A.; Nishizawa, Y.; Hirai, A.; Shinozaki, K.; Sugiura, M.
#journal Mol. Gen. Genet. (1989) 217:185-194
#title The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.

#cross-references MUID:89364698

#accession S05136
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-215 ##label HIR
##cross-references EMBL:X15901; NID:g11957; PID:g669082
##experimental_source cv. Nihonbare

COMMENT This cytochrome is one of the components of a specific stoichiometric cytochrome b6-f complex that contains two molecules of cytochrome b6, one cytochrome f and one nonheme iron-sulfur center.

GENETICS

#gene	petB
#map_position	CP1232-71237,72049-72690
#genome	chloroplast
#introns	2/3

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology

KEYWORDS chloroplast; chromoprotein; electron transfer; heme; iron; oxidoreductase; photosynthesis; thylakoid

FEATURE

15-215	#domain cytochrome b6 homology ##label CB6\
86,202	#binding_site heme iron (His) (axial ligands) #status predicted
100,187	#binding_site heme iron (His) (axial ligands) #status predicted

SUMMARY #length 215. #molecular_weight 24182 #checksum 9304

Query Match 5.8%; Score 113; DB 1; Length 215;
 Best Local Similarity 23.5%; Pred. No. 8.32e-02;
 Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTEANFGWLI-R-SV-HRWSASMMVLMILHVFVYLTGGFKKP 113
 | : :: :| :||::| :|| | :| :| :| :| :| :| :| :|

Qy 132 YIQMSIDSNISLHVHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWVTGVVLAVLTASFGVTGYS 137
 | :| ||:| :| :| :

Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 5

ENTRY S09186 #type complete
 TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
 cytochrome b6 (form 2) - barley chloroplast
 ORGANISM #formal_name chloroplast Hordeum vulgare #common_name barley
 DATE 07-Jun-1990 #sequence_revision 02-Aug-1994 #text_change
 05-Sep-1997

ACCESSIONS S09186; JN0348
 REFERENCE S04100

#authors Reverdatto, S.V.; Andreeva, A.V.; Buryakova, A.A.;
 Chakhmakhcheva, O.G.; Efimov, V.A.
 #journal Nucleic Acids Res. (1989) 17:2859-2860
 #title Nucleotide sequence of the 5.2 kbp barley chloroplast DNA
 fragment, containing psbB-psbH-petB-petD gene cluster.
 #cross-references MUID:89240047
 #accession S09186
 ##molecule_type DNA
 ##residues 1-215 ##label REV
 ##cross-references EMBL:X14107; NID:g11593; PID:e274048; PID:g1617031

GENETICS

#gene petB
 #genome chloroplast
 #introns 2/3

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology
 KEYWORDS alternative splicing; chloroplast; chromoprotein; electron
 transfer; heme; iron; oxidoreductase; photosynthesis;
 thylakoid

FEATURE

15-215 #domain cytochrome b6 homology #label CB6
 86,187 #binding_site heme iron, low potential (His) (axial
 ligands) #status predicted
 100,202 #binding_site heme iron, high potential (His) (axial
 ligands) #status predicted

SUMMARY #length 215 #molecular-weight 24166 #checksum 9436

Query Match 5.8%; Score 113; DB 1; Length 215;
 Best Local Similarity 23.5%; Pred. No. 8.32e-02;
 Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 57 YYRPTVTEAFSSVQYIMTEANFGWLI-R-SV-HRWSASMMVLMILHVFVYLTGGFKKP 113
 | : :: :| :||::| :|| | :| :| :| :| :| :| :|

Qy 132 YIQMSIDSNISLHVHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 114 REL-TWVTGVVLAVLTASFGVTGYS 137
 | :| ||:| :| :| :

Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 6

ENTRY S04149 #type complete
 TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
 cytochrome b6 (form 1) - barley chloroplast
 ORGANISM #formal_name chloroplast Hordeum vulgare #common_name barley
 DATE 07-Jun-1990 #sequence_revision 02-Aug-1994 #text_change
 05-Sep-1997

ACCESSIONS S04149; JN0381
 REFERENCE S04100
 #authors Reverdatto, S.V.; Andreeva, A.V.; Buryakova, A.A.;
 Chakhmakhcheva, O.G.; Efimov, V.A.

#journal Nucleic Acids Res. (1989) 17:2859-2860
 #title Nucleotide sequence of the 5.2 kbp-barley-chloroplast-DNA---
 fragment, containing psbB-psbH-petB-petD gene cluster.

#cross-references MUID:89240047

#accession S04149

##molecule_type DNA

##residues 1-232 ##label REV

##cross-references EMBL:X14107; NID:g11593; PID:g11596

GENETICS

#gene petB
 #genome chloroplast

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology
 KEYWORDS alternative splicing; chloroplast; chromoprotein; electron
 transfer; heme; iron; oxidoreductase; photosynthesis;
 thylakoid

FEATURE

32-232 #domain cytochrome b6 homology #label CB6
 103,204 #binding_site heme iron, low potential (His) (axial
 ligands) #status predicted
 117,219 #binding_site heme iron, high potential (His) (axial
 ligands) #status predicted

SUMMARY #length 232 #molecular-weight 26078 #checksum 4328

Query Match 5.8%; Score 113; DB 1; Length 232;
 Best Local Similarity 23.5%; Pred. No. 8.32e-02;
 Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 74 YYRPTVTEAFSSVQYIMTEANFGWLI-R-SV-HRWSASMMVLMILHVFVYLTGGFKKP 130
 | : :: :| :||::| :|| | :| :| :| :| :|

Qy 132 YIQMSIDSNISLHVHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189

Db 131 REL-TWVTGVVLAVLTASFGVTGYS 154
 | :| ||:| :| :| :

Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 7

ENTRY S58581 #type complete
 TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
 cytochrome b6 - maize chloroplast

ORGANISM #formal_name chloroplast Zea mays #common_name maize
 DATE 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change
 08-Sep-1997

ACCESSIONS S58581

REFERENCE S58531

#authors Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
 J. Mol. Biol. (1995) 251:614-628
 #title Complete sequence of the maize chloroplast genome: gene
 content, hotspots of divergence and fine tuning of genetic
 information by transcript editing.

#accession S58581

##status nucleic acid sequence not shown; translation not shown
 ##molecule_type DNA
 ##residues 1-234 ##label MAI
 ##cross-references EMBL:X86563; NID:g902200; PID:g902251
 ##note the nucleotide sequence was submitted to the EMBL Data
 Library, April 1995

GENETICS

#gene petB
 #genome chloroplast
 #introns 2/3

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology
 KEYWORDS chloroplast; electron transfer; heme; membrane-associated
 complex; oxidoreductase; photosynthesis; thylakoid

FEATURE

34-234 #domain cytochrome b6 homology #label CB6

SUMMARY #length 234 #molecular-weight 26182 #checksum 5835

Query Match 5.8%; Score 113; DB 2; Length 234;
 Best Local Similarity 23.5%; Pred. No. 8.32e-02;
 Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db 76 YYRPTVTEAFSSVQYIMTEANFGWLI-R-SV-HRWSASMMVLMILHVFVYLTGGFKKP 132

Qy 132 YIQMSIDSNISLVLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189
 Db 133 REL-TWVTGVVLAVLTASFGVTGYS 156
 | : | ||::| ::| :| ::| :| ::| :| ::| :| ::| :|
 Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 8
 ENTRY CBNT6 #type complete
 TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
 ALTERNATE NAMES cytochrome b563
 ORGANISM #formal_name chloroplast Nicotiana tabacum #common_name common tobacco
 DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 04-Oct-1996
 ACCESSIONS A00162
 REFERENCE A00149
 #authors Sugiura, M.
 #submission submitted to the EMBL Data Library, August 1986
 #accession A00162
 #molecule_type DNA
 ##residues 1-215 ##label SUG
 #experimental_source cv. Bright Yellow 4
 REFERENCE A38013
 #authors Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Zaita, N.; Chunwongse, J.; Obokata, J.; Yamaguchi-Shinozaki, K.; Ohto, C.; Torazawa, K.; Meng, B.Y.; Sugita, M.; Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdo, N.; Shimada, H.; Sugiura, M.
 #journal EMBO J. (1986) 5:2043-2049
 #title The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression.
 #contents annotation; gene organization, sites, features
 COMMENT This cytochrome is one of the components of a specific stoichiometric cytochrome b6-f complex that contains two molecules of cytochrome b6, one cytochrome f, and one nonheme iron-sulfur center.
 GENETICS
 #gene petB
 #genome chloroplast
 #introns 2/3
 CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology
 KEYWORDS chloroplast; chromoprotein; electron transfer; heme; iron; oxidoreductase; photosynthesis; thylakoid
 FEATURE
 15-215 #domain cytochrome b6 homology #label CB6
 86,202 #binding_site heme iron (His) (axial ligands) #status predicted
 100,187 #binding_site heme iron (His) (axial ligands) #status predicted
 SUMMARY #length 215 #molecular-weight 24136 #checksum 9633
 Query Match 5.7%; Score 111; DB 1; Length 215;
 Best Local Similarity 22.4%; Pred. No. 1.44e-01;
 Matches 19; Conservative 28; Mismatches 32; Indels 6; Gaps 6;
 Db 57 YYRPTVTEAFASVQYIMTEANFGWL-R-SV-HRWSASMMVLLMILHVFRVYLGGFKKP 113
 | : | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 132 YIQMSIDSNISLVLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMFLSVYKAFVMETFVHL 189
 Db 114 REL-TWVTGVVLAVLTASFGVTGYS 137
 | : | ||::| ::| :| ::| :|
 Qy 190 CSLGSWARLDARAVVTGLLALKHFG 214

RESULT 9
 ENTRY S52970 #type complete
 TITLE NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - honeybee mitochondrion (SGC4)
 ORGANISM #formal_name mitochondrion Apis mellifera #common_name

honeybee
 DATE 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 21-Aug-1998
 ACCESSIONS S52970
 REFERENCE S52960
 #authors Crozier, R.H.; Crozier, Y.C.
 #journal Genetics (1993) 133:97-117
 #title The mitochondrial genome of the honeybee *Apis mellifera*: complete sequence and genome organization.
 #accession S52970
 #molecule_type DNA
 ##residues 1-167 ##label CRO
 ##cross-references EMBL:L06178; NID:g336279; PID:g829009
 #experimental_source ligustica
 GENETICS
 #genome mitochondrion
 #genetic_code SGC4
 #start_codon ATT
 CLASSIFICATION #superfamily NADH dehydrogenase (ubiquinone) chain 6
 KEYWORDS membrane-associated complex; mitochondrion; NAD; oxidoreductase
 SUMMARY #length 167 #molecular-weight 19971 #checksum 6545
 Query Match 5.5%; Score 106; DB 2; Length 167;
 Best Local Similarity 29.9%; Pred. No. 5.58e-01;
 Matches 20; Conservative 17; Mismatches 25; Indels 5; Gaps 5;
 Db 11 IFMSSLISMILTIY-LNNIFNSPSMILLIYLYSISIYMSLMMFT-MCSMNSLLILMILIVP 68
 | : | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 147 IVASAQWVMI-TRYDLYHNFRPAVLLLMFLSVYKAFV-METFVHLCSLGSWARLDARAV- 203
 Db 69 LSGMLIM 75
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 204 VTGLLAL 210

RESULT 10
 ENTRY S21253 #type complete
 TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
 ALTERNATE NAMES cytochrome b6 - Chlamydomonas reinhardtii chloroplast
 ORGANISM #formal_name chloroplast Chlamydomonas reinhardtii
 DATE 03-Feb-1994 #sequence_revision 02-Aug-1994 #text_change 05-Sep-1997
 ACCESSIONS S21253; S16917
 REFERENCE S20938
 #authors Huang, C.; Liu, X.Q.
 #journal Plant Mol. Biol. (1992) 18:985-988
 #title Nucleotide sequence of the frxC, petB and trnL genes in the chloroplast genome of *Chlamydomonas reinhardtii*.
 #cross-references MUID:92256821
 #accession S21253
 #status translation not shown
 #molecule_type DNA
 ##residues 1-215 ##label HUA
 ##cross-references EMBL:X62905; NID:g12497; PID:g12499
 REFERENCE S16916
 #authors Bueschlen, S.; Choquet, Y.; Kuras, R.; Wollman, F.A.
 #journal FEBS Lett. (1991) 284:257-262
 #title Nucleotide sequences of the continuous and separated petA, petB and petD chloroplast genes in *Chlamydomonas reinhardtii*.
 #cross-references MUID:91285146
 #accession S16917
 #molecule_type DNA
 ##residues 1-215 ##label BOE
 ##cross-references EMBL:X72918; NID:g603530; PID:g288909
 GENETICS
 #gene petB
 #genome chloroplast
 CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology
 KEYWORDS chloroplast; chromoprotein; electron transfer; heme; iron; oxidoreductase; photosynthesis; thylakoid
 FEATURE

Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.;
 Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.;
 Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R.;
 Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwanji, N.; Caruso,
 A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.;
 McDougall, S.; Shimer, G.; Goyal, A.; Pietrovoski, S.;
 Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
 J.; Reeve, J.N.
#journal J. Bacteriol. (1997) 179:7135-7155
#title Complete genome sequence of Methanobacterium
 thermoautotrophicum Delta H: functional analysis and
 comparative genomics.
#cross-references MUID:98037514
#accession B69031
##status preliminary; nucleic acid sequence not shown;
 translation not shown
##molecule_type DNA
##residues 1-212 **##label** MTH
#cross-references GB:AE000890; GB:AE000666; NID:g2622331; PID:g2622340
##experimental_source strain Delta H
GENETICS
#gene MTH1229
CLASSIFICATION #superfamily Methanococcus jannaschii conserved hypothetical
 protein MJ0805
SUMMARY #length 212 #molecular-weight 23956 #checksum 2161

 Query Match 5.48; Score 105; DB 2; Length 212;
 Best Local Similarity 31.58; Pred. No. 7.28e-01;
 Matches 23; Conservative 17; Mismatches 27; Indels 6; Gaps 6;

 Db 44 AWALSELGKGSSIIITWIGPMVDVKNIVDYEVELEIRSEBVL-HFIVEHFDE-QPSSLRL 101
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 Qy 105 GWATAEL-IMSRCIPLWVGARGI-EF-DWKYIQMSIDSNSLIVHYIVASAQVWMTRYDL 161

 Db 102 AYHRQRILVLLM 114
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 Qy 162 -YHNPRPAVLLM 173

RESULT 14
ENTRY CBLV6 #type complete
TITLE plastoquinol--plastocyanin reductase (EC 1.10.99.1)
 cytochrome b6 - liverwort (*Marchantia polymorpha*)
 chloroplast
ORGANISM #formal_name chloroplast *Marchantia polymorpha*
DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
 04-Oct-1996
ACCESSIONS S01552; S02432; A00163
REFERENCE S01529
#authors Fukuzawa, H.; Kohchi, T.; Sano, T.; Shirai, H.; Umesono, K.;
 Inokuchi, H.; Ozeki, H.; Ohyama, K.
#journal J. Mol. Biol. (1988) 203:333-351
#title Structure and organization of *Marchantia polymorpha*
 chloroplast genome. III. Gene organization of the large
 single copy region from rbcL to trnI(CAU).
#cross-references MUID:89068687
#accession S01552
##molecule_type DNA
##residues 1-215 **##label** FUK
#cross-references EMBL:X04465
REFERENCE A38014
#authors Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.;
 Sano, S.; Umesono, K.; Shiki, Y.; Takeuchi, M.; Chang, Z.;
 Aota, S.; Inokuchi, H.; Ozeki, H.
#journal Nature (1986) 322:572-574
#title Chloroplast gene organization deduced from complete sequence
 of liverwort *Marchantia polymorpha* chloroplast DNA.
#contents annotation; gene organization, sites, features
REFERENCE S02432
#authors Fukuzawa, H.; Yoshida, T.; Kohchi, T.; Okumura, T.; Sawano,
 Y.; Ohyama, K.
#journal FEBS Lett. (1987) 220:61-66
#title Splicing of group II introns in mRNAs coding for cytochrome

b6 and subunit IV in the liverwort *Marchantia polymorpha* chloroplast genome. Exon specifying a region coding for two genes with the spacer region.

#accession S02432
 ##status not compared with conceptual translation
 ##molecule_type mRNA
 ##residues 1-8 ##label FUW

GENETICS
 #gene petB
 #genome chloroplast
 #introns 2/3

CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology

KEYWORDS chloroplast; chromoprotein; electron transfer; heme; iron; oxidoreductase; photosynthesis; thylakoid

FEATURE
 15-215 #domain cytochrome b6 homology #label CB6
 86,187 #binding_site heme iron, low potential (His) (axial ligands) #status predicted
 100,202 #binding_site heme iron, high potential (His) (axial ligands) #status predicted

SUMMARY #length 215 #molecular-weight 24307 #checksum 8453

Query Match 5.4%; Score 105; DB 1; Length 215;
 Best Local Similarity 22.7%; Pred. No. 7.28e-01;
 Matches 15; Conservative 21; Mismatches 24; Indels 6; Gaps ...6;

Db 57 YYRPTVTEAFSSVQYIMTEVNFGWLI-R-SV-HRWSASMMVLMMILHIFRVYLTGGFKKP 113
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 Qy 132 YIQMSIDSNSLVLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMPLSVYKAFVMETFVHL 189

Db 114 REL-TW 118
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 Qy 190 CSLGSW 195

RESULT 15

ENTRY S73262 #type complete
 TITLE cytochrome b6 - red alga (*Porphyra purpurea*) chloroplast
 ORGANISM #formal_name chloroplast *Porphyra purpurea*
 DATE 19-Mar-1997 #sequence_revision 09-May-1997 #text_change
 24-Apr-1998

ACCESSIONS S73262
 REFERENCE S73108
 #authors Reith, M.; Munholland, J.
 #journal Plant Mol. Biol. (1995) 13:333-335
 #title Complete nucleotide sequence of the *Porphyra purpurea* chloroplast genome.
 #accession S73262
 #status preliminary; nucleic acid sequence not shown;
 translation not shown
 ##molecule_type DNA
 ##residues 1-215 ##label REI
 ##cross-references EMBL:U38804; NID:g1276652; PID:g1276807
 ##note the nucleotide sequence was submitted to the EMBL Data Library, October 1995

GENETICS
 #gene petB
 #genome chloroplast
 CLASSIFICATION #superfamily cytochrome b6; cytochrome b6 homology
 KEYWORDS chloroplast; thylakoid

FEATURE
 15-215 #domain cytochrome b6 homology #label CB6
 SUMMARY #length 215 #molecular-weight 24224 #checksum 9699

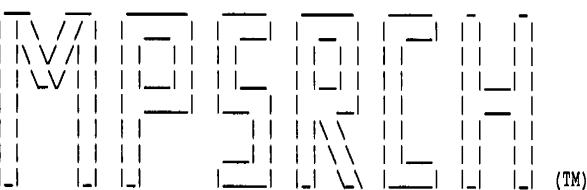
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 Best Local Similarity 22.7%; Pred. No. 9.48e-01;
 Matches 15; Conservative 20; Mismatches 25; Indels 6; Gaps 6;

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 | : :: : : | : ||:: : | : | : | : :: : | : || : :: : |
 Qy 132 YIQMSIDSNSLVLHYIVASAQV-WMITRYDLYHNFRPAVL-LLMPLSVYKAFVMETFVHL 189

Db 114 REL-TW 118

Qy 190 CSLGSW 195

Search completed: Fri Jan 22 18:00:22 1999
Job time : 19 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 22 18:03:07 1999; MasPar time 3.58 Seconds
 597.255 Million cell updates/sec

Tabular output not generated.

Title: >US-09-162-597-3
 Description: (1-245) from US09162597.pep
 Perfect Score: 1940
 Sequence: 1 MTLFHFGNCFALAYFPYFIT.....GLVSQTLMLYLPASLQLVLVK 245

Scoring table: PAM 150
 Gap 11

Searched: 92929 seqs, 8738560 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-issued
 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 31.166; Variance 148.701; scale 0.210

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	94	4.8	772	2 PCT-US95-0	Sequence 2, Applicatio	1.66e+01
2	94	4.8	772	1 US-08-258-	Sequence 2, Applicatio	1.66e+01
3	89	4.6	349	1 US-08-118-	Sequence 71, Applicati	3.57e+01
4	89	4.6	349	2 PCT-US93-0	Sequence 71, Applicati	3.57e+01
5	87	4.5	307	1 US-08-948-	Sequence 3, Applicatio	4.82e+01
6	87	4.5	417	1 US-08-553-	Sequence 2, Applicatio	4.82e+01
7	85	4.4	201	3 5489533-3	Patent No. 5489533.	6.50e+01
8	85	4.4	252	2 PCT-US95-1	Sequence 103, Applicat	6.50e+01
9	85	4.4	274	3 5489533-2	Patent No. 5489533.	6.50e+01
10	85	4.4	274	3 5512660-2	Patent No. 5512660.	6.50e+01
11	84	4.3	316	1 US-08-118-	Sequence 46, Applicati	7.54e+01
12	84	4.3	316	2 PCT-US93-0	Sequence 46, Applicati	7.54e+01
13	83	4.3	346	2 PCT-US96-1	Sequence 2, Applicatio	8.75e+01
14	83	4.3	363	1 US-08-148-	Sequence 2, Applicatio	8.75e+01
15	83	4.3	363	1 US-08-148-	Sequence 3, Applicatio	8.75e+01
16	83	4.3	380	2 PCT-US93-1	Sequence 40, Applicati	8.75e+01
17	83	4.3	380	1 US-08-153-	Sequence 40, Applicati	8.75e+01
18	84	4.3	494	2 PCT-US94-0	Sequence 4, Applicatio	7.54e+01
19	84	4.3	494	1 US-08-464-	Sequence 4, Applicatio	7.54e+01
20	84	4.3	2368	1 US-08-198-	Sequence 15, Applicati	7.54e+01
21	82	4.2	225	3 5436139-4	Patent No. 5436139.	1.01e+02
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23	82	4.2	226	3 5196194-21	Patent No. 5196194.	1.01e+02

24	82	4.2	226	2 PCT-US96-1	Sequence 14, Applicati	1.01e+02
25	82	4.2	226	3 5198348-1	Patent No. 5198348.	1.01e+02
26	82	4.2	226	1 US-08-378-	Sequence 3, Applicatio	1.01e+02
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28	82	4.2	277	3 5164485-2	Patent No. 5164485.	1.01e+02
29	82	4.2	279	1 US-07-688-	Sequence 30, Applicati	1.01e+02
30	82	4.2	279	2 PCT-US91-0	Sequence 29, Applicat	1.01e+02
31	82	4.2	281	1 US-08-458-	Sequence 214, Applicat	1.01e+02
32	82	4.2	281	2 US-08-105-	Sequence 214, Applicat	1.01e+02
33	82	4.2	351	2 PCT-US96-1	Sequence 4, Applicatio	1.01e+02
34	82	4.2	361	2 PCT-US93-0	Sequence 4, Applicatio	1.01e+02
35	82	4.2	389	1 US-08-709-	Sequence 216, Applicat	1.01e+02
36	82	4.2	389	1 US-08-709-	Sequence 219, Applicat	1.01e+02
37	82	4.2	389	1 US-08-105-	Sequence 219, Applicat	1.01e+02
38	82	4.2	389	1 US-08-458-	Sequence 216, Applicat	1.01e+02
39	82	4.2	389	1 US-08-458-	Sequence 219, Applicat	1.01e+02
40	82	4.2	389	1 US-08-105-	Sequence 216, Applicat	1.01e+02
41	82	4.2	395	3 5196194-18	Patent No. 5196194.	1.01e+02
42	82	4.2	397	2 PCT-US96-1	Sequence 6, Applicatio	1.01e+02
43	82	4.2	502	1 US-08-496-	Sequence 4, Applicatio	1.01e+02
44	82	4.2	502	1 US-08-466-	Sequence 10, Applicati	1.01e+02
45	82	4.2	995	2 PCT-US95-0	Sequence 14, Applicati	1.01e+02

ALIGNMENTS

RESULT	1	ID	PCT-US95-07391A-2	STANDARD;	PRT;	772 AA.
XX		AC	XXXXXX			
XX		DT				
XX		DE	Sequence 2, Application PC/TUS9507391A			
XX		CC	Sequence 2, Application PC/TUS9507391A			
CC		GENERAL INFORMATION:				
CC		APPLICANT:	IBEX TECHNOLOGIES and			
CC		APPLICANT:	ZIMMERMANN, Joseph			
CC		TITLE OF INVENTION:	Nucleic Acid Sequences And Expression			
CC		TITLE OF INVENTION:	Systems For Heparinase II And Heparinase III Derived Fr			
CC		TITLE OF INVENTION:	Flavobacterium heparinum			
CC		NUMBER OF SEQUENCES:	26			
CC		CORRESPONDENCE ADDRESS:				
CC		ADDRESSEE:	Hale and Dorr			
CC		STREET:	1455 Pennsylvania Avenue, N.W.			
CC		CITY:	Washington, D.C.			
CC		COUNTRY:	U.S.A.			
CC		ZIP:	20004			
CC		COMPUTER READABLE FORM:				
CC		MEDIUM TYPE:	Floppy disk			
CC		COMPUTER:	IBM PC compatible			
CC		OPERATING SYSTEM:	PC-DOS/MS-DOS			
CC		SOFTWARE:	PatentIn Release #1.0, Version #1.25			
CC		CURRENT APPLICATION DATA:				
CC		APPLICATION NUMBER:	PCT/US95/07391A			
CC		FILING DATE:	09-JUNE-1995			
CC		CLASSIFICATION:				
CC		PRIOR APPLICATION DATA:				
CC		APPLICATION NUMBER:	08/258,639			
CC		FILING DATE:	10 JUNE 1994			
CC		ATTORNEY/AGENT INFORMATION:				
CC		NAME:	BAKER, Hollie L.			
CC		REGISTRATION NUMBER:	31,321			
CC		REFERENCE/DOCKET NUMBER:	104385.116PCT			
CC		TELECOMMUNICATION INFORMATION:				
CC		TELEPHONE:	(202)942-8400			
CC		TELEFAX:	(202)942-8484			
CC		INFORMATION FOR SEQ ID NO: 2:				
CC		SEQUENCE CHARACTERISTICS:				
CC		LENGTH:	772 amino acids			
CC		TYPE:	amino acid			
CC		TOPOLOGY:	linear			

Sun Jan 24 11:29:01 1999

US-09-162-597-3.ra1

Page 2

CC MOLECULE TYPE: protein
 SQ SEQUENCE 772 AA; 87638 MW; 3109034 CN;

Query Match 4.8%; Score 94; DB 2; Length 772;
 Best Local Similarity 26.1%; Pred. No. 1.66e+01;
 Matches 23; Conservative 25; Mismatches 35; Indels 5; Gaps 3;

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Qy 66 DFIGEFMKASVDV-ADLIGLNVLMSRNA--GKGEYKIMVAALGWAT--AELIMSRCIPLW 120

Db 154 MVTGAIIVDWCYDQLKPEEKTRFKAFV 181
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Qy 121 VGARGIEFDWKYIQMSIDSNISLVHYIV 148

RESULT 2
 ID US-08-258-639A-2 STANDARD; PRT; 772 AA.

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AC XXXXX

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DE Sequence 2, Application US/08258639A

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CC Sequence 2, Application US/08258639A

CC Patent No. 5681733

CC GENERAL INFORMATION:

CC APPLICANT: Su, Hongsheng
 CC APPLICANT: Blain, Francoise
 CC APPLICANT: Bennett, Clark
 CC APPLICANT: Gu, Kangfu
 CC APPLICANT: Zimmermann, Joseph
 CC APPLICANT: Musil, Roy

CC TITLE OF INVENTION: Nucleic Acid Sequences And Expression

CC TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From

CC TITLE OF INVENTION: Flavobacterium heparinum

CC NUMBER OF SEQUENCES: 26

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Hale and Dorr
 CC STREET: 1455 Pennsylvania Avenue, N.W.
 CC CITY: Washington, D.C.
 CC COUNTRY: U.S.A.
 CC ZIP: 20004

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/258,639A

CC FILING DATE: 10 JUNE 1994

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Healey, William J.
 CC REGISTRATION NUMBER: 36,160
 CC REFERENCE/DOCKET NUMBER: 104385.116

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (202)942-8400

CC TELEFAX: (202)942-8484

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 772 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 772 AA; 87638 MW; 3109034 CN;

Query Match 4.8%; Score 94; DB 1; Length 772;
 Best Local Similarity 26.1%; Pred. No. 1.66e+01;
 Matches 23; Conservative 25; Mismatches 35; Indels 5; Gaps 3;

Db 94 DFRFYFNQKGLTVRVELMALNYLMTKDPKGREATSIIDTLETATPKPAGDISRGIGLF 153

Qy 66 DFIGEFMKASVDV-ADLIGLNVLMSRNA--GKGEYKIMVAALGWAT--AELIMSRCIPLW 120

Db 154 MVTGAIIVDWCYDQLKPEEKTRFKAFV 181
 : : | :| | | : : : | : |

Qy 121 VGARGIEFDWKYIQMSIDSNISLVHYIV 148

RESULT 3
 ID US-08-118-270-71 STANDARD; PRT; 349 AA.
 XX
 AC XXXXX
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 DT
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 DE Sequence 71, Application US/08118270
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 CC Sequence 71, Application US/08118270
 CC Patent No. 5508384
 CC GENERAL INFORMATION:
 CC APPLICANT: Murphy, Randall B.
 CC APPLICANT: Schuster, David I.
 CC TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 CC TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 CC NUMBER OF SEQUENCES: 348

CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: BROWDY AND NEIMARK
 CC STREET: 419 Seventh Street, N.W., Suite 300
 CC CITY: Washington
 CC STATE: D.C.
 CC COUNTRY: USA
 CC ZIP: 20004
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/118,270
 CC FILING DATE: 09-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/943,236
 CC FILING DATE: 10-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Townsend, Kevin G.
 CC REGISTRATION NUMBER: 34,033
 CC REFERENCE/DOCKET NUMBER: MURPHY-2A
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-628-5197
 CC TELEFAX: 202-737-3528
 CC TELEX: 248633
 CC INFORMATION FOR SEQ ID NO: 71:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 349 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 SQ SEQUENCE 349 AA; 39913 MW; 695896 CN;

Query Match 4.6%; Score 89; DB 1; Length 349;
 Best Local Similarity 20.5%; Pred. No. 3.57e+01;
 Matches 18; Conservative 29; Mismatches 38; Indels 3; Gaps 3;

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Qy 125 GIEFDWKYIQMSIDSNISLVHYIVASAQVWMITRYDLYHNFRPAVLLMFL-SVIKAFVM 183

Db 154 DPFPPEPADL-FWKYLIDATFILLYLLPL 180
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Qy 184 ETFVHLCLSGSWARLDARA-VVTGLLAL 210

Sun Jan 24 11:29:01 1999

US-09-162-597-3.ra1

Page 3

RESULT 4

ID PCT-US93-08528-71 STANDARD; PRT; 349 AA.

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AC XXXXXX

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DE Sequence 71, Application PC/TUS9308528

XX

CC Sequence 71, Application PC/TUS9308528

CC GENERAL INFORMATION:

CC APPLICANT: New York University

CC TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

CC TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

CC NUMBER OF SEQUENCES: 348

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: BROWDY AND NEIMARK

CC STREET: 419 Seventh Street, N.W., Suite 300

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: USA

CC ZIP: 20004

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/08528

CC FILING DATE: 09-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/943,236

CC FILING DATE: 10-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Townsend, Kevin G.

CC REGISTRATION NUMBER: 34,033

CC REFERENCE/DOCKET NUMBER: MURPHY-2 PCT

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 202-628-5197

CC TELEFAX: 202-737-3528

CC TELEX: 248633

CC INFORMATION FOR SEQ ID NO: 71:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 349 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

SQ SEQUENCE 349 AA; 39913 MW; 695896 CN;

Query Match 4.6%; Score 89; DB 2; Length 349;

Best Local Similarity 20.5%; Pred. No. 3.57e+01;

Matches 18; Conservative 29; Mismatches 38; Indels 3; Gaps 3;

Db 94 AIAVDRHQVIMPLKPRISITKGVIYIAVIWVMTFFSLPHAIQKLFKYSEDIVRSCL 153

Qy 125 GIEFDWKYIQMSIDSNSLHVYTIVASAQWVWMTRYDLYHNFRPAVLLMFL-SVYKAFVM 183

Db 154 DPFPEPADL-FWKYLDIATFILLYLLPL 180

Qy 184 ETFVHLCISLGWSWARLDARA-VVTGLLAL 210

RESULT 5

ID US-08-948-616-3 STANDARD; PRT; 307 AA.

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AC XXXXXX

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DT

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DE Sequence 3, Application US/08948616

XX

CC Sequence 3, Application US/08948616

CC Patent No. 5840539

CC GENERAL INFORMATION:

CC APPLICANT: Hillman, Jennifer L.

CC APPLICANT: Lal, Preeti

CC APPLICANT: Shah, Purvi

CC APPLICANT: Corley, Neil C.

CC TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS

CC NUMBER OF SEQUENCES: 11

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Incyte Pharmaceuticals, Inc.

CC STREET: 3174 Porter Drive

CC CITY: Palo Alto

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 94304

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FastSEQ for Windows Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/948,616

CC FILING DATE: Herewith

CC CLASSIFICATION: 530

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER:

CC FILING DATE:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Billings, Lucy J.

CC REGISTRATION NUMBER: 36,749

CC REFERENCE/DOCKET NUMBER: PF-0409 US

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 650-855-0555

CC TELEFAX: 650-845-4166

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 3:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 307 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC IMMEDIATE SOURCE:

CC LIBRARY: LUNGUTU07

CC CLONE: 2607662

SQ SEQUENCE 307 AA; 34947 MW; 494826 CN;

Query Match 4.5%; Score 87; DB 1; Length 307;

Best Local Similarity 26.9%; Pred. No. 4.82e+01;

Matches 14; Conservative 14; Mismatches 22; Indels 2; Gaps 2;

Db 240 YCYLLVYYTG-WRNVKSFLTFGLICLCNM-YLYELRNLWQLFPHTVGAFV 289

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Qy 21 YKCSGLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTWEGGIYDFIGEFM 72

RESULT 6

ID US-08-553-703A-2 STANDARD; PRT; 417 AA.

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AC XXXXXX

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DT

XX

DE Sequence 2, Application US/08553703A

XX

CC Sequence 2, Application US/08553703A

CC Patent No. 5795767

CC GENERAL INFORMATION:

CC APPLICANT: MARU, ISAFUMI

CC APPLICANT: OHTA, YASUHIRO

CC APPLICANT: TSUKADA, YOJI

CC TITLE OF INVENTION: EPIMERASE

CC NUMBER OF SEQUENCES: 9

CC CORRESPONDENCE ADDRESS:

Sun Jan 24 11:29:01 1999

US-09-162-597-3.ra1

Page 4

CC ADDRESSEE: Knobbe, Martens, Olson & Bear
 CC STREET: 620 Newport Center Drive, 16th Floor
 CC CITY: Newport Beach
 CC STATE: CA
 CC COUNTRY: U.S.A.
 CC ZIP: 92660
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Diskette
 CC COMPUTER: IBM Compatible
 CC OPERATING SYSTEM: DOS
 CC SOFTWARE: FastSEQ Version 1.5
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/553,703A
 CC FILING DATE: 30-NOV-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Altman, Daniel E
 CC REGISTRATION NUMBER: 34,115
 CC REFERENCE/DOCKET NUMBER:
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 714-760-0404
 CC TELEFAX: 714-760-9502
 CC TELEX:
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 417 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC FRAGMENT TYPE: N-terminal
 SQ SEQUENCE 417 AA; 47746 MW; 847834 CN;

Query Match 4.5%; Score 87; DB 1; Length 417;
 Best Local Similarity 23.8%; Pred. No. 4.82e+01;
 Matches 15; Conservative 18; Mismatches 26; Indels 4; Gaps 4;

Db 19 LDRVVAFWMEHSHDQEHHGFFTCLGREGRVYDDLKYVWLQGRQVWMYCRLYRTFERRHA 78
 : | ::|: :: | : :: :: : | : | ||| || : || |

Qy 113 MSRCIPLWVG-ARGIEFDWKYIQMSIDSNI-SLVHYI-VASAQVWMITR-YDLYHNFRPA 168

Db 79 QLL 81
 ||

Qy 169 VLL 171

RESULT 7
 ID 5489533-3 STANDARD; PRT; 218 AA.

XX XXXXXX

XX DT 01-JAN-1900

XX DE Patent No. 5489533.

XX Patent No. 5489533
 CC APPLICANT: SPRINGER, TIMOTHY A.; STAUNTON, DONALD E.;
 CC DUSTIN, MICHAEL L.
 CC TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
 CC ICAM-2

CC NUMBER OF SEQUENCES: 16
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/384,814
 CC FILING DATE: 06-FEB-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 89,3075
 CC FILING DATE: 12-JUL-1995
 CC APPLICATION NUMBER: 89,307
 CC FILING DATE: 12-JUL-1993
 CC APPLICATION NUMBER: 454,294

CC FILING DATE: 22-DEC-1989
 CC APPLICATION NUMBER: 45,963
 CC FILING DATE: 04-MAY-1987
 CC APPLICATION NUMBER: 115,798
 CC FILING DATE: 02-NOV-1987
 CC APPLICATION NUMBER: 155,943
 CC FILING DATE: 16-FEB-1988
 CC APPLICATION NUMBER: 189,815
 CC FILING DATE: 03-MAY-1988
 CC APPLICATION NUMBER: 250,446
 CC FILING DATE: 28-SEP-1988
 CC SEQ ID NO:3:
 CC LENGTH: 201
 SQ SEQUENCE 218 AA; 24265 MW; 273614 CN;

Query Match 4.4%; Score 85; DB 3; Length 201;
 Best Local Similarity 28.3%; Pred. No. 6.50e+01;
 Matches 17; Conservative 14; Mismatches 25; Indels 4; Gaps 4;

Db 52 QWKHYLVSNISHDTVLQCHFTCSKGQESMNSNVYQPPRQVILTLQPTLVAVGKSFTE 111
 :||| : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 129 DWK-YIQMSIDSNSL-VHYIVASAQVWMITRDLYHNFRPAVLLM-FL-SVYKAFVME 184

RESULT 8
 ID PCT-US95-14442A-103 STANDARD; PRT; 252 AA.

XX AC XXXXXX

XX DT

XX

DE Sequence 103, Application PC/TUS9514442A
 XX

CC Sequence 103, Application PC/TUS9514442A

CC GENERAL INFORMATION:

CC APPLICANT: Grieve, Robert B.
 CC APPLICANT: Rushlow, Keith E.
 CC APPLICANT: Hunter, Shirley Wu
 CC APPLICANT: Frank, Glenn R.
 CC APPLICANT: Heath, Andrew W.
 CC APPLICANT: Yamaka, Miles Yamanaka
 CC APPLICANT: Arfsten, Ann
 CC APPLICANT: Dale, Beverly
 CC APPLICANT: Stiegler, Gary
 CC TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
 CC TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
 CC TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
 CC TITLE OF INVENTION: MOLECULES, AND USES THEREOF
 CC NUMBER OF SEQUENCES: 119

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Sheridan Ross & McIntosh
 CC STREET: 1700 Lincoln Street, Suite 3500
 CC CITY: Denver
 CC STATE: Colorado
 CC COUNTRY: USA
 CC ZIP: 80203

CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/14442A

CC FILING DATE:

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Gary J. Connell
 CC REGISTRATION NUMBER: 32,020
 CC REFERENCE/DOCKET NUMBER:
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (303) 863-9700
 CC TELEFAX: (303) 863-0223
 CC INFORMATION FOR SEQ ID NO: 103:

Sun Jan 24 11:29:01 1999

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Page 6

CC REGISTRATION NUMBER: 34,033
 CC REFERENCE/DOCKET NUMBER: MURPHY-2A
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-628-5197
 CC TELEFAX: 202-737-3528
 CC TELEX: 248633
 CC INFORMATION FOR SEQ ID NO: 46:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 316 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 SQ SEQUENCE 316 AA; 36040 MW; 553094 CN;

Query Match 4.3%; Score 84; DB 1; Length 316;
 Best Local Similarity 37.0%; Pred. No. 7.54e+01;
 Matches 10; Conservative 10; Mismatches 5; Indels 2; Gaps 2;

Db 43 ASADLIIA-CGLPFWAITIANNFDWLF 68
 ::::|::| :| :|| : :|| :
 Qy 107 ATAELIMSRC-IPLWVGARGIEFDWKY 132

RESULT 12
 ID PCT-US93-08528-46 STANDARD; PRT; 316 AA.

XX
 AC XXXXXX
 XX

DT
 XX

DE Sequence 46, Application PC/TUS9308528
 XX

CC Sequence 46, Application PC/TUS9308528
 CC GENERAL INFORMATION:

CC APPLICANT: New York University
 CC TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

CC TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

CC NUMBER OF SEQUENCES: 348

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: BROWDY AND NEIMARK

CC STREET: 419 Seventh Street, N.W., Suite 300

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: USA

CC ZIP: 20004

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/08528

CC FILING DATE: 09-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/943,236

CC FILING DATE: 10-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Townsend, Kevin G.

CC REGISTRATION NUMBER: 34,033

CC REFERENCE/DOCKET NUMBER: MURPHY-2 PCT

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 202-628-5197

CC TELEFAX: 202-737-3528

CC TELEX: 248633

CC INFORMATION FOR SEQ ID NO: 46:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 316 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

SQ SEQUENCE 316 AA; 36040 MW; 553094 CN;

Query Match 4.3%; Score .84; DB 2; Length 316;
 Best Local Similarity 37.0%; Pred. No. 7.54e+01;
 Matches 10; Conservative 10; Mismatches 5; Indels 2; Gaps 2;

Db 43 ASADLIIA-CGLPFWAITIANNFDWLF 68
 ::::|::| :| :|| : :|| :
 Qy 107 ATAELIMSRC-IPLWVGARGIEFDWKY 132

RESULT 13
 ID PCT-US96-10602-2 STANDARD; PRT; 346 AA.

XX
 AC XXXXXX
 XX

DT
 XX

DE Sequence 2, Application PC/TUS9610602
 XX

CC Sequence 2, Application PC/TUS9610602

CC GENERAL INFORMATION:

CC APPLICANT: The General Hospital Corporation

CC TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION

CC NUMBER OF SEQUENCES: 14

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Fish & Richardson P.C.

CC STREET: 225 Franklin Street

CC CITY: Boston

CC STATE: MA

CC COUNTRY: USA

CC ZIP: 02110-2804

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US96/10602

CC FILING DATE:

CC CLASSIFICATION:

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 60/017,814

CC FILING DATE: 20-JUN-1995

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Clark, Paul T.

CC REGISTRATION NUMBER: 30,162

CC REFERENCE/DOCKET NUMBER: 00786/282001

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 617/542-5070

CC TELEFAX: 617/542-8906

CC TELEX: 200154

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 346 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 346 AA; 40128 MW; 678897 CN;

Query Match 4.3%; Score 83; DB 2; Length 346;

Best Local Similarity 35.1%; Pred. No. 8.75e+01;

Matches 13; Conservative 10; Mismatches 10; Indels 4; Gaps 4;

Db 192 NGFRWMLRRPIIYLVLLLC-LIFLVL-LDWKGLI 226
 ::::|::| :| :|| :| :|| :| :|| :

Qy 30 NAF-WKCWQAGVTLFVQL-CKMLFLATFFPTWEGGI 64

RESULT 14
 ID US-08-148-209A-2 STANDARD; PRT; 363 AA.

XX
 AC XXXXXX

Sun Jan 24 11:29:01 1999

US-09-162-597-3.ra1

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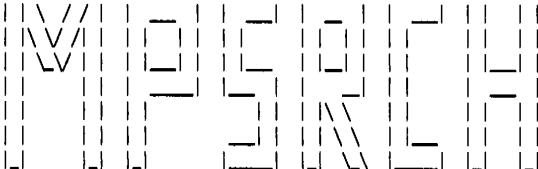
XX
DT
XX
DE Sequence 2, Application US/08148209A
XX
CC Sequence 2, Application US/08148209A
CC Patent No. 5556780
CC GENERAL INFORMATION:
CC APPLICANT: Dzau, Victor J
CC APPLICANT: Mukoyama, Masashi
CC TITLE OF INVENTION: TYPE-2 ANGIOTENSIN II RECEPTOR AND GENE
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
CC STREET: 4 Embarcadero Center, Suite 3400
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94111-4187
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/148,209A
CC FILING DATE: 05-NOV-1993
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Rowland, Bertram I
CC REGISTRATION NUMBER: 20,015
CC REFERENCE/DOCKET NUMBER: A-58491-1/BIR
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 781-1989
CC TELEFAX: (415) 398-3249
CC TELEX: 910 277299
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 363 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 363 AA; 41330 MW; 722740 CN;

Query Match 4.3%; Score 83; DB 1; Length 363;
Best Local Similarity 32.6%; Pred. No. 8.75e+01;
Matches 14; Conservative 11; Mismatches 14; Indels 4; Gaps 4;

Db 172 CLSSLPTFY-FRD-VRT-IEYLGVNACIMAFPPEKYAQWSAGI 211
| |:: : : |: |:: : || | | | : :: | :||
Qy 23 C-SGLSEYNNAFWKCVQAGVTYLFVQLCKMLFLATFFPTWEGGI 64

Search completed: Fri Jan 22 18:03:21 1999
Job time : 14 secs.

RESULT 15
ID US-08-148-209A-3 STANDARD; PRT; 363 AA.
XX
AC *****
XX
DE Sequence 3, Application US/08148209A
XX
CC Sequence 3, Application US/08148209A
CC Patent No. 5556780
CC GENERAL INFORMATION:
CC APPLICANT: Dzau, Victor J
CC APPLICANT: Mukoyama, Masashi
CC TITLE OF INVENTION: TYPE-2 ANGIOTENSIN II RECEPTOR AND GENE
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
CC STREET: 4 Embarcadero Center, Suite 3400
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94111-4187
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/148,209A
CC FILING DATE: 05-NOV-1993
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Rowland, Bertram I
CC REGISTRATION NUMBER: 20,015
CC REFERENCE/DOCKET NUMBER: A-58491-1/BIR
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 781-1989
CC TELEFAX: (415) 398-3249
CC TELEX: 910 277299
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 363 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 363 AA; 41330 MW; 725910 CN;


 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 22 17:58:21 1999; MasPar time 8.04 Seconds
 492.876 Million cell updates/sec

Tabular output not generated.

Title: >US-09-162-597-3
 Description: (1-245) from US09162597.pep
 Perfect Score: 1940
 Sequence: 1 MTLFHFGNCFALAYFPYFIT.....GLVSQTLMYLFPASLQLVLK 245

Scoring table: PAM 150
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0.8
 Listing first 45 summaries

Database: a-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 33.119; Variance 147.508; scale 0.225

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
.	.	1	99	5.1	237	22	W20142	H. pylori inner membr	1.14e+01
.	.	2	98	5.1	422	21	R97722	Mouse inositol polyph	1.34e+01
.	.	3	98	5.1	497	22	W20821	H. pylori cell envelo	1.34e+01
.	.	4	95	4.9	1353	19	R99251	Murine adenylate cycl	2.17e+01
.	.	5	94	4.8	772	15	R89264	Heparinase-II.	2.55e+01
.	.	6	94	4.8	843	13	R67760	Lys-aminopeptidase Pe	2.55e+01
.	.	7	91	4.7	359	22	W20927	H. pylori surface or	4.11e+01
.	.	8	92	4.7	521	21	W14445	CarA gene product.	3.51e+01
.	.	9	89	4.6	349	19	W02722	G-protein coupled mou	5.64e+01
.	.	10	89	4.6	349	16	R48750	G-protein coupled mou	5.64e+01
.	.	11	87	4.5	174	3	R21412	NADH dehydrogenase 6.	7.70e+01
.	.	12	87	4.5	293	21	W14481	Ranp-1.	7.70e+01
.	.	13	87	4.5	417	16	R79929	Porcine acylglucosami	7.70e+01
.	.	14	88	4.5	558	2	P70429	Murine neuroleukin.	6.59e+01
.	.	15	85	4.4	152	29	W48271	Rat ninjurin 1.	1.05e+02
.	.	16	85	4.4	252	20	W01210	Serine protease PfSP1	1.05e+02
.	.	17	85	4.4	274	1	R06836	Intercellular adhesio	1.05e+02
.	.	18	85	4.4	1477	22	W10424	Saccharomyces cerevis	1.05e+02

19	85	4.4	1477	13	R67691	S. cerevisiae scaur2R	1.05e+02
20	86	4.4	1989	18	R99640	Peripheral nervous sys	8.99e+01
21	86	4.4	4473	20	R97244	Virulence gene cluste	8.99e+01
22	84	4.3	236	1	P81992	Hepatitis B viral sur	1.22e+02
23	84	4.3	316	19	W02697	G-protein coupled rat	1.22e+02
24	84	4.3	316	16	R48725	G-protein coupled rat	1.22e+02
25	83	4.3	346	21	W09046	WHV core-surface fusi	1.42e+02
26	83	4.3	363	13	R66934	Mouse AT2 receptor.	1.42e+02
27	83	4.3	380	11	R53750	Seven transmembrane r	1.42e+02
28	83	4.3	391	29	W38453	Wild-type human homol	1.42e+02
29	84	4.3	422	22	W20249	H. pylori transmembra	1.22e+02
30	84	4.3	426	22	W20934	H. pylori surface or	1.22e+02
31	84	4.3	494	28	W42996	Putative mature potas	1.22e+02
32	84	4.3	494	16	R90765	Human K+ channel 2 ma	1.22e+02
33	84	4.3	1233	29	W34536	Nudaurelia beta virus	1.22e+02
34	84	4.3	1233	29	W41935	Nudaurelia beta-like	1.22e+02
35	84	4.3	2368	26	W26663	Yeast checkpoint cont	1.22e+02
36	84	4.3	2510	6	R29527	HCV antigen T7N1-30.	1.22e+02
37	84	4.3	3011	4	R22154	NANBV Hutch c59 isola	1.22e+02
38	83	4.3	3085	23	W19701	ATM mutant G9170C.	1.42e+02
39	82	4.2	226	7	R33252	HBsAg encoded by pGPD	1.66e+02
40	82	4.2	250	2	R11496	RP142/HBsAg.	1.66e+02
41	82	4.2	351	21	W09047	Plasmid pHBV DN inser	1.66e+02
42	82	4.2	558	2	P70430	Human neuroleukin.	1.66e+02
43	82	4.2	658	27	W27666	Streptococcus pneumon	1.66e+02
44	82	4.2	724	27	W36797	Novel human gene, des	1.66e+02
45	82	4.2	898	21	W14777	Granulosis virus infe	1.66e+02

ALIGNMENTS

RESULT 1
 ID W20142 standard; protein; 237 AA.
 AC W20142;
 DT 08-JUL-1997 (first entry)
 DE H. pylori inner membrane protein, 14455461.aa.
 KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 OS Helicobacter pylori.
 FH Key Location/Qualifiers
 FT misc_difference 3
 FT /note= "encoded by YCC"
 FT misc_difference 130
 FT /note= "encoded by RCG"
 FT misc_difference 183
 FT /note= "encoded by GSY"
 PN W09640893-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U09122.
 PR 07-JUN-1995; US-487032.
 PR 01-APR-1996; US-630405.
 PA (ASTR) ASTRA AB.
 PI Berglindh OT, Smith D, Mellgaard BL;
 DR WPI; 97-052306/05.
 DR N-PSDB; T67385.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 56; Pages 365; 1481pp; English.
 CC The present sequence is a Helicobacter pylori inner membrane protein.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds,
 CC useful as potential H. pylori life cycle activators or inhibitors.
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from
 CC overlapping contigs generated by mechanically shearing the bacterial
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
 CC and the predicted coding regions defined by computer evaluation. To
 CC identify likely H. pylori antigens for vaccine development, the amino
 CC acid sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide

CC production, e.g. in E. coli hosts.
SQ Sequence 237 AA;

```

Query Match      5.1%; Score 99; DB 22; Length 237;
Best Local Similarity 25.2%; Pred. No. 1.14e+01;
Matches 32; Conservative 30; Mismatches 54; Indels 11; Gaps 9;

Db    23 vglcsylligfiwyhk-ksannasialeafvmrritdiglmqilif-wnfgtlqykev fsm 80
.     ||| |::: : :: | |:: : :||: ||: | |::| :|:
Qy   45 VQLCKMLPLATFFPTWEGGIYDFIGEFMKASV-DVADLIGLNLVMSRNAGKGEYKIMVA 103

Db    81 innadysmlfyisvflfigamgkqsagfpmtwlanamegptpvsalihattmvtagvyli 140
| | :: : ||| | :| | + | + :| :| :| :| :| :| :| :
Qy  104 LGWATAELIMSRCIPLWVGARG--IEF--D-WKYIQMSIDSNS-LVH-YIVASAQVWMI 156

Db    141 iranply 147
| :|
Qy  157 TRYD-LY 162

```

RESULT 2

ID R97722 standard; Protein; 422 AA.
AC R97722;
DT 29-APR-1997 (first entry)
DE Mouse inositol polyphosphate binding protein IP4-BP.
KW Synaptogamin; antagonist; inhibitor; neurotransmitter; hormone;
KW calcium release; inositol; polyphosphate; pentakisphosphate;
KW hexakisphosphate; tetrakisphosphate; binding protein; IP4-BP;
KW PCR primer; polymerase chain reaction; murine.
CC Mus musculus

OS Mus musculus.
 FH Key Location/Qualifiers
 FT peptide 315..346
 FT /label= synaptogamin_II
 FT /note= "part of C2A domain"
 PN J08092290-A.
 PD 09-APR-1996

PS Example 8; Page 14-15; 19pp; Japanese.
CC Degenerate primers (see T29741 and T29742) were designed based on
CC peptide fragments from the inositol polyphosphate binding protein
CC IP4BP isolated from ddY mouse cerebellum. The primers were used for
CC PCR amplification of the mouse IP4BP gene (see T29743). The C2A
CC domain at the C-terminal end of IP4BP contains the synaptogamin II
CC peptide. A consensus sequence was obtained from a comparison of
CC synaptogamin peptides from a variety of species. Peptides comprising
CC the consensus motif (see R97721) are able to bind to inositol
CC tetrakisphosphate, inositol pentakisphosphate and inositol
CC hexakisphosphate; such peptides can inhibit neurotransmitter release
CC and hormone release and are calcium inhibitors.
SO Sequence 422 AA.

Query Match 5.1%; Score 98; DB 21; Length 422;
Best Local Similarity 48.5%; Pred. No. 1.34e+01;
Matches 16; Conservative 6; Mismatches 8; Indels 3; Gaps 3;

Db 62 plppwa-liamavvaglllltccf-cickkccc 92
Qy 191 SLGSWARLDAVARVVTGLALKH-FGPVCRRQC 222

RESULT 3

ID W20821 standard; Protein; 497 AA.
AC W20821;
DT 16-JUL-1997 (first entry)
DE H. pylori cell envelope inner membrane protein 11c11603orf16.
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;

KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
OS Helicobacter pylori.
PN WO9640893-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09122.
PR 07-JUN-1995; US-487032.
PR 01-APR-1996; US-630405.
PA (ASTR) ASTRA AB.
PI Berglindh OT, Smith D, Mellgaard BL;
DR WPI; 97-052306/05.
DR N-PSDB; T68074.
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
PS Claim 56; Page 1226-1227; 1481pp; English.
CC The present sequence shows a Helicobacter pylori cell envelope
CC inner membrane protein.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
SQ Sequence 497 AA;

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Query Match      5.1%; Score 98; DB 22; Length 497;
Best Local Similarity 25.2%; Pred. No. 1.34e+01;
Matches 32; Conservative 30; Mismatches 54; Indels 11; Gaps 9;

Db   156 vglcsylligfwyhk-ksannasieafvnmritdglmngjilif-wnfgtlqykev fsm 213
| || |::: : :: | | :: : |::: |::: |::: | : | : |::: |:
Qy   45 VQLCKMLPLATFFPTWEGGIYDFIGEFPMKASV-DVADLIGLNLVMSRNAGKGEYKIMVA 103

Db   214 lnnadysmlyfisvflfligamgksaqfpmphtwlanamegptpvsalihaatmvtagvyli 273
| | :: : |::: | | : | | : | : |::: |::: | : | |:
Qy   104 LGWATAELIMSRICPLWWVGARG--IEF--D-WKYIQMSIDSNSIS-LVHY-IVASAQVWMI 156

Db   274 iranply 280
| : ||
Qy   157 TRYD-LY 162

```

RESULT 4

ID R99251 standard; Protein; 1353 AA.

AC R99251;

DT 01-DEC-1996 (first entry)

DE Murine adenylate cyclase 9.
KW Adenylate cyclase; calcineurin; cellular metabolism; tumour;
KW neurological; cardiovascular; endocrine; respiratory; bone; kidney;
KW pregnancy; gut; therapy.

OS Mus cookii.
FH Key Location/Qualifiers
FT modified_site 27
FT /label= C-kinase
FT /note= "putative protein kinase C phosphorylation
FT site"
FT modified_site 84
FT /label= CAM_kinase-II
FT /note= "putative CAM kinase II phosphorylation
FT site"
FT modified_site 85
FT /label= A-kinase
FT /note= "putative protein kinase A phosphorylation
FT site"
FT modified_site 94

FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	187	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	200	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	201	
FT	/label= A-kinase	
FT	/note= "putative protein kinase A phosphorylation site"	
FT modified_site	261	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	266	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	303	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	304	
FT	/label= A-kinase	
FT	/note= "putative protein kinase A phosphorylation site"	
FT modified_site	356	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	358	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	370	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	432	
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FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	436	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT domain	503..610	
FT modified_site	581	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	588	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	596	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	597	
FT	/label= A-kinase	
FT	/note= "putative protein kinase A phosphorylation site"	
FT modified_site	619	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
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FT modified_site	690	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	719	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	732	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	761	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	763	
FT	/label= A-kinase	
FT	/note= "putative protein kinase A phosphorylation site"	
FT modified_site	765	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	837	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	885	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	919	
FT	/label= A-kinase	
FT	/note= "putative protein kinase A phosphorylation site"	
FT modified_site	971	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	972	
FT	/label= A-kinase	
FT	/note= "putative protein kinase A phosphorylation site"	
FT modified_site	972	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	1002	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	1019	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	1002	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	1105	
FT	/label= C-kinase	
FT	/note= "putative protein kinase C phosphorylation site"	
FT modified_site	1194	
FT	/label= CAM_kinase-II	
FT	/note= "putative CAM kinase II phosphorylation site"	
FT modified_site	1199	
FT	/label= Casein_kinase-II	
FT	/note= "putative casein kinase II phosphorylation site"	
FT modified_site	1211	

KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 OS Helicobacter pylori.

PN W09640893-A1.

PD 19-DEC-1996.

PF 06-JUN-1996; D09122.

PR 07-JUN-1995; US-487032.

PR 01-APR-1996; US-630405.

PA (ASTR) ASTRA AB.

PI Berglindh OT, Smith D, Mellgaerd BL;

DR WPI; 97-052306/05.

DR N-PSDB; W20927.

PT Helicobacter pylori nucleic acid sequences and related

PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
infection, and to detect Helicobacter

PS Claim 73; Page 1324-1325; 1481pp; English.

CC The present sequence is a H. pylori surface or membrane protein likely
to contain seven or more membrane spanning regions.

CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.

SQ Sequence 359 AA;

Query Match 4.7%; Score 91; DB 22; Length 359;

Best Local Similarity 34.3%; Pred. No. 4.11e+01;

Matches 12; Conservative 13; Mismatches 7; Indels 3; Gaps 3;

Db 242 slvp-avggaliwipiaiyelyhghvneaifivly 275

||| :||: :| : | : ||| : |:::::

Qy 142 SLVHYIVASAQVWM-ITRYDLYH-NFRPAVLLMF 174

RESULT 8

ID W14445 standard; Protein; 521 AA.

AC W14445;

DT 17-MAY-1997 (first entry)

DE CarA gene product.

KW carbapenem; carR; carA; carB; carC; carD; carE; carF; carG; carH;

KW biosynthesis; antibiotic; beta-lactamase inhibitor; regulatory.

OS Erwinia carotovora.

PN W09532294-A1.

PD 30-NOV-1995.

PF 18-MAY-1995; G01125.

PR 20-MAY-1994; GB-010142.

PA (UYNO-) UNIV NOTTINGHAM. PA (UYWA-) UNIV WARWICK.

PI Bycroft BW, Cox ARJ, Holden MTG, McGowan SJ, Porter LE;

PI Saimond GPC, Sebaihia M, Stewart GSA, Williams P;

DR WPI; 96-020587/02.

DR N-PSDB; T09700.

PT New genes encoding enzymes involved in carbapenem biosynthesis -

PT useful for isolating other carbapenem synthesising genes and
PT producing carbapenem in heterologous organisms

PS Disclosure; Fig 4; 31pp; English.

CC W14445-52 are the protein products of the car genes (carA-H) which are
CC involved in the biosynthesis of carbapenem, an antibiotic which acts as
CC a beta-lactamase inhibitor. The car biosynthetic genes are regulated by
CC the carR gene product (W14444), a positive activator of the biosynthetic
CC genes which functions in trans. The car genes can be used to identify
CC homologous genes in bacteria and fungi, while products of the genes may
CC be used to raise antibodies used to detect clones (in a Streptomyces
CC library) that express cross-reactive protein.

SQ Sequence 521 AA;

Query Match 4.7%; Score 92; DB 21; Length 521;

Best Local Similarity 36.4%; Pred. No. 3.51e+01;

Matches 12; Conservative 6; Mismatches 14; Indels 1; Gaps 1;

Db 64 kcemergratayligslynrtfliglagvwegeay 96

||| ::| :||: | : || : ||| |

Qy 34 KC-VQAGVTLYFVQLCKMLPLATFFPTWEGGIY 65

RESULT 9

ID W02722 standard; peptide; 349 AA.

AC W02722;

DT 13-NOV-1996 (first entry)

DE G-protein coupled mouse glucocorticoid-induced receptor.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;

KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;

KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;

KW odorant; cytomegalovirus; serotonergic.

OS Mus musculus.

PN US5508384-A.

PD 16-APR-1996.

PF 10-SEP-1992; 943236.

PR 10-SEP-1992; US-943236.

PR 09-SEP-1993; US-118270.

PA (UYNY) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;

DR WPI; 96-208785/21.

PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
PT for treating schizophrenia

PS Disclosure; Column 163-166; 184pp; English.

CC Proteins W02657-W02730 represent a range of G-protein coupled receptor

(GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,

CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,

CC odorant, cytomegaloviral and other GPR proteins. The receptor proteins

CC were used to design polypeptides, pref. based on the transmembrane

CC domains, for use in G-protein coupled receptor ligand binding assays.

CC The polypeptide fragments retain biological activity such as binding a

CC GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W02999

CC for examples of polypeptide fragments). The polypeptide fragments can

CC be used in compositions for treating subjects suffering from a pathology

CC related to a GPR abnormality e.g. a psychotic disorder such as

CC schizophrenia.

SQ Sequence 349 AA;

Query Match 4.6%; Score 89; DB 19; Length 349;

Best Local Similarity 20.5%; Pred. No. 5.64e+01;

Matches 18; Conservative 29; Mismatches 38; Indels 3; Gaps 3;

Db 94 aiavdrhqvimplkprisitkgviyaviwwmtffslphaicqklftfkysedivrslo1 153

:| :| :||: :| :| :| :| :| :| :| :| :| :| :| :

Qy 125 GIEFDWKYIQMSIDSNSIISLWHYIVASAQVWMTRYDLYHNFRPAVLLMFL-SVYKAFMV 183

Db 154 dpfpepadl-fwyldiatfllylpl 180

:| | | | || :| :| :| :

Qy 184 ETFVHLCSLGSWARLDARA-VVTGLLAL 210

RESULT 10

ID R48750 standard; Protein; 349 AA.

AC R48750;

DT 07-JUN-1996 (first entry)

DE G-protein coupled mouse glucocorticoid-induced receptor protein.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;

KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;

KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;

KW rhodopsin; opsin; odorant; cytomegalovirus.

OS Mus musculus.

PN W09405695-A1.

PD 17-MAR-1994.

PF 09-SEP-1993; U08528.

PR 10-SEP-1992; US-943236.

PA (UYNY) UNIV NEW YORK STATE.

PI Murphy RB, Schuster DI;

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DR WPI; 94-101120/12.
 PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding GPR ligands or modulating GPR binding
 PS Disclosure; Page 125-126; 160pp; English.
 CC Proteins R48685-R48758 represent a range of G-protein coupled receptor proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see R48759-R48758, R50569-R50807 and R89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 SQ Sequence 349 AA;

Query Match 4.6%; Score 89; DB 16; Length 349;
 Best Local Similarity 20.5%; Pred. No. 5.64e+01;
 Matches 18; Conservative 29; Mismatches 38; Indels 3; Gaps 3;

Db 94 aiavdrhqvimplkprisitkgviyiaiviwmmtffslphaicqklftfkysedivrscl 153
 :| :| :| :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 125 GIEFDWKYIQMSIDSNSLHYIVASAQVWMITRYDLYHNFRPAVLLMFL-SVYKAFVM 183
 Db 154 dpfppepadl-fwkyldiatfillyllpl 180
 :| :| :| | || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 184 ETFVHLCISLGWSWARLDARA-VVTGLLAL 210

RESULT 11
 ID R21412 standard; Protein; 174 AA.
 AC R21412;
 DT 01-APR-1992 (first entry)
 DE NADH dehydrogenase 6.
 KW Pneumonia; assay; AIDS; immunosuppressed.
 OS Pneumocystis carinii.
 PN WO9119005-A.
 PD 12-DEC-1991.
 PF 31-MAY-1991; G00869.
 PR 01-JUN-1990; GB-012196.
 PA (ISIS-) ISIS INNOVATION LTD.
 PI Wakefield AE, Hopkin JM, Moxon ER;
 DR WPI; 92-007487/01.
 DR N-PSDB; Q20065.
 PT New DNA sequences which act as oligo:nucleotide primers - for assaying DNA sample from respiratory secretion of a patient infected with P carinii
 PS Claim 3; Fig 3; 42pp; English.
 CC The amino acid sequence is that of P. carinii NADH dehydrogenase 6 which was translated from DNA from plasmid pAZ112. See also R21409-R21413 and R20056.
 SQ Sequence 174 AA;

Query Match 4.5%; Score 87; DB 3; Length 174;
 Best Local Similarity 31.0%; Pred. No. 7.70e+01;
 Matches 13; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Db 99 sslvftlylsplpreimekyshlfyswernrilnpsveil 140
 ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 167 PAVLLLMFLSYKAFVMETFVHLCISLGWSA-RLDARAVVTGL 207

RESULT 12
 ID W14481 standard; Protein; 293 AA.
 AC W14481;
 DT 28-MAY-1997 (first entry)
 DE Ranp-1.
 KW ranp-1; 5'-nucleotidase consensus sequence; nervous damage; 5'-AMP; treat; improved activity; organ; 5'-adenosine monophosphate.
 OS Rattus rattus.
 PN J09040697-A.

DR 10-FEB-1997.
 PT 27-JUL-1995; 192082.
 PR 27-JUL-1995; JP-192082.
 PA (SHIO) SHIONOGI & CO LTD.
 DR WPI; 97-175708/16.
 DR N-PSDB; T62693.
 PT Protein containing 5'-nucleotidase consensus sequence which specifically binds AMP - is useful for treatment of nervous diseases
 PS Claim 2; Page 10-11; 13pp; Japanese.
 CC The sequence is that of ranp-1 which contains a 5'-nucleotidase consensus sequence. The DNA expression is enhanced when there is nervous damage.
 CC The protein enhances 5'-nucleotidase activity and binds specifically with 5'-AMP. Nervous diseases can be treated and the activity of various organs can be improved by controlling the expression of the DNA and the protein.
 SQ Sequence 293 AA;

Query Match 4.5%; Score 87; DB 21; Length 293;
 Best Local Similarity 26.2%; Pred. No. 7.70e+01;
 Matches 16; Conservative 17; Mismatches 21; Indels 7; Gaps 5;

Db 64 lfsllpg-flfqfipfmrkkyiqdkpetfegwkclkgilfnhffiqpligctyyftfe 122
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 3 LEHFGNCPALAYPPYFITYKC-SGLSE-YNAFWKCVQAGV-TYLFVQL---CKMLFLATP 56
 Db 123 f 123
 |
 Qy 57 F 57

RESULT 13
 ID R79929 standard; Protein; 417 AA.
 AC R79929;
 DT 09-MAY-1996 (first entry)
 DE Porcine acylglucosamine-2-epimerase mutant.
 KW Porcine; acylglucosamine-2-epimerase; N-acetylmannosamine;
 KW N-acetylneurameric acid; renin-binding; enzymatic production;
 KW mutant.
 OS Sus scrofa.
 FH Key Location/Qualifiers
 FT misc_difference 23
 FT /note= "wild type Met subst. with Val"
 FT misc_difference 27
 FT /note= "wild type Leu subst. with Met"
 FT misc_difference 33
 FT /note= "wild type Arg subst. with Gln"
 FT misc_difference 45
 FT /note= "wild type Asp subst. with Glu"
 FT misc_difference 71
 FT /note= "wild type Lys subst. with Thr"
 FT misc_difference 72
 FT /note= "wild type Leu subst. with Phe"
 FT misc_difference 76
 FT /note= "wild type His subst. with Arg"
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 FT misc_difference 78
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 FT /note= "wild type Glu subst. with Gln"
 FT misc_difference 94
 FT /note= "wild type His subst. with Tyr"
 FT misc_difference 101
 FT /note= "wild type Glu subst. with Gly"
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 FT /note= "wild type Ser Substd. with Thr"
 FT misc_difference 137
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 FT misc_difference 141
 FT /note= "wild type Ala subst. with Val"
 FT misc_difference 145

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FT /note= "wild type Ser subst. with Thr"
 FT misc_difference 149
 /note= "wild type Asp subst. with Glu"
 FT misc_difference 159
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 FT misc_difference 162
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 FT misc_difference 174
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 FT misc_difference 205
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 FT misc_difference 208
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 FT misc_difference 249
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 FT misc_difference 275
 /note= "wild type Thr subst. with Lys"
 FT misc_difference 282
 /note= "wild type Arg subst. with His"
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 FT misc_difference 301
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 FT misc_difference 329
 /note= "wild type Glu subst. with Asp"
 FT misc_difference 334
 /note= "wild type Ala subst. with Val"
 FT misc_difference 363
 /note= "wild type Asn subst. with Ser"
 FT misc_difference 371
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 FT misc_difference 395
 /note= "wild type Leu subst. with Pro"
 FT misc_difference 395
 /note= "wild type Ser subst. with Gly"
 FT misc_difference 401
 /note= "wild type Leu subst. with Pro"
 FT misc_difference 403..417
 /note= "C-terminal addition to the wild type
 sequence"
 PN WO9526399-A1.

PD 05-OCT-1995.
 PF 24-MAR-1995; J00541.
 PR 25-MAR-1994; JP-056271.
 PR 09-SEP-1994; JP-216333.
 PA (MARU) MARUKIN SHOYU KK.
 PI Maru I, Ohta Y, Tsukada Y;
 DR WPI; 95-351320/45.
 PT Recombinant acyl:glucosamine-2-epimerase with renin-binding activity
 - useful in enzymic production of N-acetyl:mannosamine and
 PT N-acetyl:neuraminic acid
 PS Claim 13; Pages 59-61; 74pp; Japanese.
 CC R79929 is a porcine acylglucosamine-2-epimerase (A2P) mutant,
 with renin-binding activity. A2P can be used for the enzymatic
 CC prodn. of N-acetylmannosamine and N-acetylneuraminic acid.
 SQ Sequence 417 AA;

Query Match 4.5%; Score 87; DB 16; Length 417;
 Best Local Similarity 23.8%; Pred. No. 7.70e+01;
 Matches 15; Conservative 18; Mismatches 26; Indels 4; Gaps 4;

Db 19 ldrvva fwme hshd qehggfftclggregrvyddlk ywlqgrqvwm ycrlyrtferfrha 78
 : | ::::| : :: | : :: :: : : | : : |||| | | : || |

Qy 113 MSRCIPLWVG-ARGIEFDWKYIQMSIDSNI-SLVHYI-VASAQVWMITR-YDLYHNFRPA 168

Db 79 qll 81
 ||
 Qy 169 VLL 171

RESULT 14
 ID P70429 standard; protein; 558 AA.
 AC P70429;
 DT 16-JAN-1991 (first entry)
 DE Murine neuroleukin.
 KW Neuroleukin; neural cells; HIV; AIDS; env gene; vaccine.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT region 1..436
 FT /label=first exon
 FT region 437..0
 FT /label=second exon
 PN W08707617-A.
 PD 17-DEC-1987.
 PF 04-JUN-1987; U01323.
 PR 05-JUN-1986; US-872332.
 PA (GENE-) Genetics Institute Inc. .
 PI Gurney ME, Knopf JL;
 DR WPI; 87-362709/51.
 DR N-PSDB; N70686.
 PT New neuroleukin protein - useful for culturing neural cells, and for
 treating human immunodeficiency virus.
 PS Claim 1; page 22; 29pp; English.
 CC Neuroleukin is a single polypeptide chain of apparent mol. wt. 56000 +/-
 CC 2000 D (by SDS-PAGE), with the ability to maintain 1/2 maximal survival
 CC of spinal or sensory neurons cultured in vitro at a neuroleukin concn. of
 CC 0.0000000125 M, and the ability to activate immunoglobulin secretion by
 CC peripheral blood lymphocytes. Neuroleukin is useful in tissue culture
 CC medium for culturing neural cells and extends the survival of sensory
 CC ganglia, brain cells and spinal neurons in culture. A portion of the DNA
 CC sequence has significant homology to portion of the HTLV III/LAV envelope
 CC protein gene, thus may be useful to treat AIDS, or in an AIDS
 CC vaccine. Its treatment of HIV infection is claimed. The protein
 CC is encoded by 2 exons.
 SQ Sequence 558 AA;

Query Match 4.5%; Score 88; DB 2; Length 558;
 Best Local Similarity 29.0%; Pred. No. 6.59e+01;
 Matches 18; Conservative 18; Mismatches 20; Indels 6; Gaps 6;

Db 269 wvgrr-ysl-wsaiglsialhvqfdhf eqllsahwm dqhf-lktpleknapvllallgi 325
 ||||| : | | : || :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 120 WVGARGIEFDWKYIQMSIDSNI-SLVHYI-VASAQVWMITR-YDLYHNFRPA 177

Db 326 w 327

Qy 178 -Y 178

RESULT 15

ID W48271 standard; Protein; 152 AA.

AC W48271;

DT 23-JUN-1998 (first entry)

DE Rat ninjurin 1.

KW Rat; ninjurin; cellular adhesion molecule; membrane bound; tumour;

KW nerve injury induced gene; inflammation; nervous system.

OS Rattus sp.

PN W09803650-A1.

PD 29-JAN-1998.

PF 24-JUL-1997; U12210.

PR 24-JUL-1996; US-672850.

PA (UNIW) UNIV WASHINGTON.

PI Araki T, Milbrandt J;

DR WPI; 98-120775/11.

DR N-PSDB; V20665.

PT New isolated nerve injury induced (ninjurin) gene - used to develop

products for treating conditions involving excessive or insufficient

cellular adhesion, e.g. inflammation or tumours

PS Claim 5; Fig 1B; 80pp; English.

CC The present sequence represents rat ninjurin 1 (nerve injury induced).

CC The ninjurin protein (NP) plays a role in axonal regeneration of

CC peripheral nervous system (PNS)-neuronal cells after injury. The

CC products can be used for developing products for treating ninjurin

CC mediated disorders including conditions involving inappropriate (i.e.

CC excessive or insufficient) cellular adhesion. Conditions involving

CC excessive cellular adhesion which may be treated include e.g.

CC inflammatory diseases such as rheumatoid arthritis, asthma, allergy

CC conditions, adult respiratory distress syndrome, inflammatory bowel

CC diseases (e.g. Crohn's disease, ulcerative colitis and regional

CC enteritis) and ophthalmic inflammatory diseases, autoimmune diseases,

CC thrombosis or inappropriate platelet aggregation conditions,

CC arteriosclerosis, reocclusion following thrombolysis, cardiovascular

CC diseases, some forms of diabetes and neoplastic disease including

CC metastasis conditions. The products can also be used to promote

CC cellular adhesion, e.g. in nerve regeneration, wound healing or

CC prosthetic implantation. The products can also be used for detection,

CC purification, diagnosis and screening assays.

SQ Sequence 152 AA;

Query Match 4.4%; Score 85; DB 29; Length 152;

Best Local Similarity 27.6%; Pred. No. 1.05e+02;

Matches 21; Conservative 19; Mismatches 31; Indels 5; Gaps 5;

Db 56 llmanasqlkavvveggnefaf-fvplvvvlisislqlqigvgvlliflv-kydlnnpkha 113

::: | | : || :: : : || | | : : : : || | : |

Qy 111 LIMSRCIPLW-VGARGIEEDWKYIQMSIDSNISLWHYI-VASAQVWMITRDLYHNFRPA 168

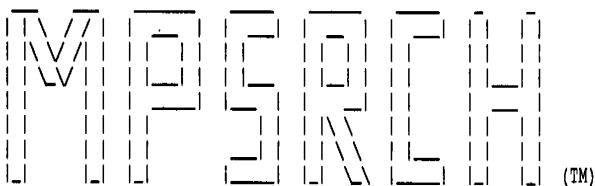
Db 114 kldflnnlatglvfii 129

| : | : | : :

Qy 169 VL-LLMFLSVYKAFVM 183

Search completed: Fri Jan 22 17:59:45 1999

Job time : 84 secs.



(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 22 18:01:16 1999; MasPar time 15.58 Seconds
782.839 Million cell updates/sec

Tabular output not generated.

Title: >US-09-162-597-3
Description: (1-245) from US09162597.pep
Perfect Score: 1940
Sequence: 1 MTLHFHGNCFALAYFPYFIT.....GLVSQTLMLYLPASLQLVLVK 245

Scoring table: PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp Rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.110; Variance 101.374; scale 0.455

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred.	No.
1	636	32.8	216	5	Q23483	COSMID ZK418.		2.66e-90		
2	119	6.1	1087	5	Q46089	1-EVIDENCE-PREDICTED B		1.50e-02		
3	113	5.8	215	8	Q36712	PETB, PETD [RNA EDITIN		8.40e-02		
4	113	5.8	232	8	Q32438	POT. ALT. PETB GENE PR		8.40e-02		
5	113	5.8	232	8	Q33298	ALTERNATE PETB GENE PR		8.40e-02		
6	113	5.8	232	8	Q36615	APOCYTOCHROME B6.		8.40e-02		
7	109	5.6	300	2	Q32730	ATTAZ PROTEIN.		2.58e-01		
8	106	5.5	271	8	Q63292	NADH DEHYDROGENASE SUB		5.80e-01		
9	105	5.4	212	1	Q27297	CONSERVED PROTEIN.		7.72e-01		
10	104	5.4	310	2	Q51297	CONSERVED HYPOTHETICAL		1.01e+00		
11	104	5.4	379	8	Q47977	CYTOCHROME B.		1.01e+00		
12	105	5.4	527	10	Q64515	YUP8H12R.2 PROTEIN.		7.72e-01		
13	104	5.4	1410	5	Q18259	SIMILARITY ALONG ENTIR		1.01e+00		
14	103	5.3	308	5	Q17615	C29F3.6.		1.32e+00		
15	102	5.3	379	8	Q47963	CYTOCHROME B.		1.73e+00		
16	102	5.3	379	8	Q47962	CYTOCHROME B.		1.73e+00		
17	102	5.3	380	8	Q48000	CYTOCHROME B (FRAGMENT		1.73e+00		
18	102	5.3	503	8	Q37612	CYTOCHROME C OXIDASE S		1.73e+00		
19	101	5.2	204	8	Q47043	CYTOCHROME B (FRAGMENT		2.25e+00		
20	101	5.2	348	8	Q47403	NADH DEHYDROGENASE SUB		2.25e+00		

21	100	5.2	348	8	Q47399	NADH DEHYDROGENASE SUB	2.92e+00
22	100	5.2	348	8	Q47398	NADH DEHYDROGENASE SUB	2.92e+00
23	101	5.2	379	8	Q47991	CYTOCHROME B.	2.25e+00
24	101	5.2	379	8	Q47965	CYTOCHROME B.	2.25e+00
25	101	5.2	379	8	Q47992	CYTOCHROME B.	2.25e+00
26	101	5.2	379	8	Q47972	CYTOCHROME B.	2.25e+00
27	101	5.2	379	8	Q47966	CYTOCHROME B.	2.25e+00
28	101	5.2	379	8	Q47974	CYTOCHROME B.	2.25e+00
29	101	5.2	379	8	Q47970	CYTOCHROME B.	2.25e+00
30	100	5.2	379	8	Q47982	CYTOCHROME B.	2.92e+00
31	101	5.2	380	8	Q47971	CYTOCHROME B.	2.25e+00
32	101	5.2	380	8	Q47976	CYTOCHROME B.	2.25e+00
33	101	5.2	380	8	Q47964	CYTOCHROME B.	2.25e+00
34	101	5.2	380	8	Q47990	CYTOCHROME B.	2.25e+00
35	101	5.2	380	8	Q47975	CYTOCHROME B.	2.25e+00
36	101	5.2	495	8	Q34463	CYTOCHROME OXIDASE SUB	2.25e+00
37	101	5.2	550	2	Q31692	PHOSPHOTRANSFERASE SYS	2.25e+00
38	101	5.2	573	2	Q69251	ENZYME I.	2.25e+00
39	99	5.1	133	8	Q47442	CYTOCHROME B (FRAGMENT	3.80e+00
40	99	5.1	247	1	Q50081	247AA LONG HYPOTHETICA	3.80e+00
41	99	5.1	345	5	Q20963	RELATED TO C. ELEGANS	3.80e+00
42	99	5.1	363	1	Q26434	PEROSAMINE SYNTHETASE.	3.80e+00
43	99	5.1	379	8	Q48001	CYTOCHROME B.	3.80e+00
44	99	5.1	379	8	Q48364	CYTOCHROME B.	3.80e+00
45	99	5.1	2206	5	P91744	VOLTAGE-DEPENDENT CALC	3.80e+00

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	216 AA.
ID	Q23483			
AC	Q23483;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	COSMID ZK418.			
GN	ZK418.5.			
OS	CAENORHABDITIS ELEGANS.			
OC	EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RX	MEDLINE; 94150718.			
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;			
RL	NATURE 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	FULTON L.;			
RL	SUBMITTED (APR-1994) TO EMBL/GENBANK/DDJB DATA BANKS.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	WATERSTON R.;			
RL	SUBMITTED (APR-1994) TO EMBL/GENBANK/DDJB DATA BANKS.			
DR	EMBL; U00047; G470373; -.			
SQ	SEQUENCE 216 AA; 23931 MW; 8B1C508A CRC32;			

Query Match 32.8%; Score 636; DB 5; Length 216;
Best Local Similarity 47.8%; Pred. No. 2.66e-90;
Matches 76; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Db 1 MSFFHFINCFLAFAPYFIVKYSGNEYSSIWKATASGGYLTLQLAKLIIATFFPAL 60
:::||||| ::||| |||::|||::|||::|||::|||::|||:

Qy	1 MTLFHFGNCALAYFPYFITYKCSGLSEYNAFWKVQAGVTYLFVQLCKMLFLATFFPTW 60
Db	61 DSEGFSIVPEFLKSSADIIDVIGLHLLMTNFLAGKGEVRFVVGGLGWFGAHSVRAHRLVV 120 :: : :: : : : : : : : : : : : : : : :
Qy	61 EGGIYDFIGEPMKAISVDADLIGLNLMWSRN -AGKGEYKIMVAALGWATAELIMSRICPL 119
Db	121 WVGARGTAFTWRWVQTSLDSSADLLVIVSLACLTWMITR 159 : : : : : : : : : : : :
Qy	120 WVGARGIEFDWKYIOMSDNSNISLVLHVYIVASAQVWMITR 158

RESULT 2
ID 046089 PRELIMINARY; PRT; 1087 AA.
AC 046089;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE 1-EVIDENCE-PREDICTED BY MATCH.
GN EG:63B12.9.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]
RP SEQUENCE FROM N.A.
RA FERRAZ C., VIDAL S., BRUN C., BUCHETON A., DEMAILLE J.G.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDJB DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA BENOS P.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDJB DATA BANKS.
DR EMBL; AL021106; E1249577; -.
SQ SEQUENCE 1087 AA; 123655 MW; C4CA9980 CRC32;

RESULT 3
ID Q36712 PRELIMINARY; PRT; 215 AA.
AC Q36712;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE PETB, PETD (RNA EDITING).
GN PETB.
OS ZEA SP.
OG CHLOROPLAST.
OC EUKARYOTA; PLANTAE; EMBRYOBIONTA; MAGNOLIOPHYTA; LILIOPSI
OC COMMELINIDAE; CYPERALES; POACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94073219.
RA FREYER R., HOCH B., NECKERMAN K., MAIER R.M., KOSSEL H.;
RL PLANT J. 4:621-629(1993).
CC -!- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C = Q +
CC FERRICYTOCHROME C.
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE N
CC BOUND TO THE PROTEIN (BY SIMILARITY).
DR EMBL; S67283; G453127; -.
DR EMBL; S67282; G453127; JOINED.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PFAM; PF00033; cytochrome_b_N.
KW CHLOROPLAST; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANS
KW HEME.
SQ SEQUENCE 215 AA: 24196 MW: C290F74A CPC32;

Query Match 5.8%; Score 113; DB 8; Length 215;
Best Local Similarity 23.5%; Pred. No. 8.40e-02;
Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db	57	YVRYPTVTEAFSSVQYIMTEANFGWLI	R-SV-HRWSASMMVLMMILHVFRVYLGGFKP-113-
	: ::	: :: :	: : : :: : :
Qy	132	YIQMSISDNISLHVYIVASAQV-WMITRVDLYHNFRPAVL-LLMPLSLVYKAFVMETFVHL	189
Db	114	REL-TWVTGVVLA VLTASFGVTGYS	137
	:	: : :: :	
Qy	190	CSLGSWARL DARA VVTG LALKHFG	214

RESULT 4
ID Q32438 PRELIMINARY; PRT; 232 AA.
AC Q32438;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE POT. ALT. PETB GENE PRODUCT.
OS HORDEUM VULGARE (BARLEY).
OG CHLOROPLAST.
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
OC CYPERALES; GRAMINEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SABARLIS;
RX MEDLINE; 89240047.
RA REVERDATTO S.V., ANDREEVA A.V., BURYAKOVA A.A., CHAKHMAKHCHEVA O.G.,
RA EFIMOV V.A.;
RL NUCLEIC ACIDS RES. 17:2859-2860(1989).
CC -!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
CC FERROCYTOCHROME C.
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
DR EMBL; X14107; G11596; -.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PFAM; PF00033; cytochrome_b_N.
KW CHLOROPLAST; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANSMEMBRANE;
KW HEME.
SQ SEQUENCE 232 AA; 26078 MW; F06F9FF4 CRC32;

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Query Match      5.8%; Score 113; DB 8; Length 232;
Best Local Similarity 23.5%; Pred. No. 8.40e-02;
Matches 20; Conservative 27; Mismatches 32; Indels 6; Gaps 6;

Db    74 YYRPTIVTEAFSSVQYIMTEANFGWLI-R-SV-HRWASASMMVLMLILHVFRVYLTCFFKKP 130
      | : : | : ||::| | : || | : | :: | : ||:| | : | : |
Qy 132 YIQMISDSNISLNVHYIIVASAQV-WMITYRDLYHNFRPAVL-LMLPLSVYKAFVMETFVHL 189

Db    131 REL-TWVTGVVLAVALTASEGVTGYS 154
      . | : | : ||:| : :: | : |
Qy 190 CSLGSWRLDARAVVTGLLALKHFG 214

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RESULT 5
ID Q33298 PRELIMINARY; PRT; 232 AA.
AC Q33298;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ALTERNATE PETB GENE PRODUCT.
GN PETB.
OS ZEA MAYS (MAIZE).
OG CHLOROPLAST.
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
OC CYPERALES; GRAMINEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88210525.
RA ROCK C.D., BARKAN A., TAYLOR W.C.;
RL CURR. GENET. 12:69-77(1987).
CC -1- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C = O + 2
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).

Sun Jan 24 11:29:04 1999

US-09-162-597-3.rspt

Page 4

RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
 RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
 RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
 RA MCDougall S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
 RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
 RL J. BACTERIOL. 179:7135-7155(1997).
 DR EMBL; AE000890; G2622340; -.
 SQ SEQUENCE 212 AA; 23956 MW; 7EB119AC CRC32;

Query Match 5.4%; Score 105; DB 1; Length 212;
 Best Local Similarity 31.5%; Pred. No. 7.72e-01;
 Matches 23; Conservative 17; Mismatches 27; Indels 6; Gaps 6;
 Db 44 AWALSELGKSSIIITWIGPMVKNIVDYEVDVELEIRSEEVL-HFIVEHFDE-QPSSLRL 101
 ::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Qy 105 GWATTEL-IMSRCIPLWVGARGI-EF-DWKYIQMSIDSNSLVLHYIVASAQVWMTRYDL 161
 ::|::|::|:
 Db 102 AYHRQRILVVMLM 114
 ::|::|::|:
 Qy 162 -YHNFRPAVLLM 173

RESULT 10
 ID 051297 PRELIMINARY; PRT; 310 AA.
 AC 051297;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE CONSERVED HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN.
 GN BB0317.
 OS BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; SPIROCHETES; SPIROCHAETALES;
 OC SPIROCHAETACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE; 98065943.
 RA FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
 RA LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWENN M.,
 RA DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
 RA PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
 RA VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
 RA UTTERBACK T., WATTHEY L., McDONALD L., ARTIACH P., BOWMAN C.,
 RA GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
 RA SMITH H.O., VENTER J.C.;
 RL NATURE 390:580-586(1997).
 DR EMBL; AE001138; G2688213; -.
 DR TIGR; BB0317; -.
 SQ SEQUENCE 310 AA; 35680 MW; C8F8F32F CRC32;

Query Match 5.4%; Score 104; DB 2; Length 310;
 Best Local Similarity 28.0%; Pred. No. 1.01e+00;
 Matches 23; Conservative 22; Mismatches 34; Indels 3; Gaps 3;

Db 229 VVFFRPYLVGLTSGLG-WSSLIVAVISGFNYVYVLFSSLFSILIEFFNNFLNINYDFKY 287
 ::|::|::|::|::|::|::|::|::|::|::|:
 Qy 12 LAYF-PYFITYKCSGLSEYNNAFWKCVQAGVTYLFVQLCKMLFLATF-FPTWEGGIYDFIG 69
 ::|::|::|::|:
 Db 288 EFIGLCQSIAIFISLFLIKARK 309
 ::|::|::|::|:
 Qy 70 EFMKASVVDALIGLNUVMSRN 91

RESULT 11
 ID 047977 PRELIMINARY; PRT; 379 AA.
 AC 047977;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE CYTOCHROME B.
 GN CYTB.
 OS THOMOMYS BOTTAE (BOTTA'S POCKET GOPHER).
 OG MITOCHONDRION.

OC EUKARYOTAE; MITOCHONDRIAL EUKARYOTES; METAZOA; CHORDATA; VERTEBRATA;
 OC MAMMALIA; EUHERIA; RODENTIA; SCIUROGNATHI; GEOMYIDAE; THOMOMYS...
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MV2 156025;
 RA SMITH M.F.;
 RL MOL. PHYLOGENET. EVOL. 9:1-14(1998).
 CC -!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
 FERROCYTOCHROME C.
 CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 DR EMBL; U65267; G2894730; -.
 DR PROSITES; PS00192; CYTOCHROME_B_HEME; 1.
 KW MITOCHONDRION; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANSMEMBRANE;
 KW HEME.
 SQ SEQUENCE 379 AA; 43115 MW; 93B942A8 CRC32;

Query Match 5.4%; Score 104; DB 8; Length 379;
 Best Local Similarity 26.2%; Pred. No. 1.01e+00;
 Matches 16; Conservative 18; Mismatches 23; Indels 4; Gaps 3;

Db 71 RDVNCGWLIRYMHANGASLFFICLYIHIGRXY-YGSY-LYNETWNVGILLFLTMATAF 128
 |::|::|::|::|::|::|::|::|::|::|::|:
 Qy 124 RGIEFDW-KYIQLMSIDSNSLVLHYIVASAQVWMTRYDLHNPRAVLLMFLSVYKAF 181
 Db 129 V 129
 |
 Qy 182 V 182

RESULT 12
 ID 064515 PRELIMINARY; PRT; 527 AA.
 AC 064515;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE YUP8H12R.2 PROTEIN.
 GN YUP8H12R.2.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC CAPPARALES; CRUCIFERAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A., VYSOTSKAIA V.S., OSBORNE B.I., SCHWARTZ J.R.,
 RA FEDERSPIEL N.A., KWAN A., TORIUMI M., YU G., OJI, O., ARAUJO R.,
 RA CHUNG E., DEWER K., DIETRICH F., ECKER J.R., MARZIALI A., OEFNER P.,
 RA DAVIS R.W.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL; AC002986; G3152576; -.
 SQ SEQUENCE 527 AA; 57750 MW; 3B215C12 CRC32;

Query Match 5.4%; Score 105; DB 10; Length 527;

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Best Local Similarity 22.9%; Pred. No. 7.72e-01;
 Matches 25; Conservative 28; Mismatches 48; Indels 8; Gaps 8;

Db 158 LTVFSPNIWVYAVLRFVNNGFRATIGTCALVLSTELVGKKWRGRVGIMSSFFGMLGFLSL 217
 | : | | | :: | : | : | : | : | : | : | : | : |
 Qy 53 LATFFPT-WEGGIYDFIGEFMKASVDVADLI-GLNLVMSRNAGK-GEYKIMVAALGWATA 109

Db 218 PL-MA-YMN-RGSSWRILYAWTISIPTIIYC-V-LVRFFVCESPRWLWV 261
 | : | : | : | : | : | : | : | : | : | : |
 Qy 110 ELIMSRCIPLWVGARGIEFDWKYIQMSIDSNSLHVHYIVASAQVWMITR 158

RESULT 13
 ID Q18259 PRELIMINARY; PRT; 1410 AA.
 AC Q18259;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE SIMILARITY ALONG ENTIRE GENE TO CALCIUM CHANNEL ALPHA PROTEINS.

GN C27F2.3.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; ACEROLAMATES; NEMATODA; SECERNENTEA; RHABDITIDA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
 RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
 RA HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
 RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
 RA RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
 RA SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPROAT J., WOHLDMAN P.,
 RL NATURE 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA KIRSTEN J.;

RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A.

RA WATERSTON R.;

RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR EMBL; U40419; G1065507; -.

DR PFAM; PF00520; ion_trans.

SQ SEQUENCE 1410 AA; 162922 MW; 57A8C35A CRC32;

Query Match 5.4%; Score 104; DB 5; Length 1410;
 Best Local Similarity 24.7%; Pred. No. 1.01e+00;
 Matches 18; Conservative 22; Mismatches 27; Indels 6; Gaps 6;

Db 913 IWMPNH-IEINSWAQLLMVCRAMRPLRVYALIP-HIRRVVV-ELCRGFR-EILLVTILLV 968
 | : | : | : | : | : | : | : | : | : | : | : |
 Qy 119 LWVGARGIEFD-WKYIQMSIDSNSLHVHYIVASAQVWMITRDLYHNFRPAVLLMFLSV 177

Db 969 VLMFIFASPFGVQL 981
 | : | : | : |

Qy 178 YKAFVMETF-VHL 189

RESULT 14
 ID 017615 PRELIMINARY; PRT; 308 AA.
 AC 017615;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

DE C29F3.6.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; ACEROLAMATES; NEMATODA; SECERNENTEA; RHABDITIDA.

RN [1]

RP SEQUENCE FROM N.A.

RA MATTHEWS L.;

RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

RN [2]

RP SEQUENCE FROM N.A.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
 RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
 RA HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
 RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
 RA RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
 RA SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPROAT J., WOHLDMAN P.,
 RL NATURE 368:32-38(1994).
 DR EMBL; Z81043; E347909; -.
 DR PFAM; PF00001; 7tm_1.
 SQ SEQUENCE 308 AA; 35499 MW; BB5A2150 CRC32;

Query Match 5.3%; Score 103; DB 5; Length 308;

Best Local Similarity 25.5%; Pred. No. 1.32e+00;

Matches 38; Conservative 40; Mismatches 59; Indels 12; Gaps 11;

Db 61 YLFY-FCFMDFLDVFLFQE-NVFIFGFLVAVFHDSVLTHFIISLNRFISVWCPIF-YKT 117
 | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 42 YLFVQLCKMLPLATF-PPTWEGGIYDF-IGEFMKASVDVADLIGLNLVMSRNAGKGEYKI 99

Db 118 MFN-LKYTKLIFAVWLISFLIGS--L-FHIVLCRIRFNADLILFTIILAPSYCPEIGRY 173
 | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 100 MVAALGWATAELIMSRICPLNVGARGIEFDWKYIQMSIDSNSLHVHYIVASAQVWMITR 159

Db 174 GDLFRN-SCIVIIMMILDWF-TLIKVKLI 200
 | : | : | : | : | : | : | : | : | : |

Qy 160 -DLYHNFRPAVLLMPLSVKAFVMETFV 187

RESULT 15

ID 047963 PRELIMINARY; PRT; 379 AA.

AC 047963;

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE CYTOCHROME B.

GN CYTB.

OS THOMOMYS BOTTAE (BOTTA'S POCKET GOPHER).

OG MITOCHONDRION.

OC EUKARYOTA; MITOCHONDRIAL EUKARYOTES; METAZOA; CHORDATA; VERTEBRATA;

OC MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; GEOMYIDAE; THOMOMYS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MVZ 166821;

RA SMITH M.F.;

RL MOL. PHYLOGENET. EVOL. 9:1-14(1998).

CC -|- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2

CC FERROCYTOCHROME C.

CC -|- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

DR EMBL; U65253; G2894702; -.

DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

KW MITOCHONDRION; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANSMEMBRANE;

KW HEME.

SQ SEQUENCE 379 AA; 43114 MW; 9E37B5B0 CRC32;

Query Match 5.3%; Score 102; DB 8; Length 379;

Best Local Similarity 27.9%; Pred. No. 1.73e+00;

Matches 17; Conservative 16; Mismatches 24; Indels 4; Gaps 3;

Db 71 RDVNFGWLIRYMHANGASLFFICLYIHIGRGY-YGSY-LYKETWNVGILLPLTMATAF 128
 | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 124 RGIEFDW--KIIQMSIDSNSLHVHYIVASAQVWMITRYDLYHNFRPAVLLMPLSVKAF 181

Db 129 V 129
 | : |

Qy 182 V 182

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